

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:14:00 ; Search time 7417.52 Seconds
(without alignments)
12559.330 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
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8: em_htc:*
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10: gb_est2:*
11: gb_htc:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	986	25.7	1798	11	AF125103	AF125103 Homo sapi
2	915.6	23.9	1785	11	AF077050	AF077050 Homo sapi
3	774.2	20.2	3533	11	AK034902	AK034902 Mus muscu
c 4	668.6	17.4	956	9	AL573494	AL573494 AL573494
5	646.8	16.9	896	14	CB204418	CB204418 AGENCOURT
6	631	16.5	871	13	BQ719894	BQ719894 AGENCOURT
7	628.8	16.4	646	14	CB467517	CB467517 733269 MA
8	625.4	16.3	627	12	BM986175	BM986175 LM24HW001
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11	614.2	16.0	822	14	CB521332	CB521332 UI-M-GH0-
12	605.2	15.8	901	13	BQ879359	BQ879359 AGENCOURT
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15	581.2	15.2	958	12	BM801698	BM801698 AGENCOURT
c 16	580	15.1	996	10	BF570468	BF570468 602186269
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c 18	568.8	14.8	598	14	CB534701	CB534701 768054 MA
19	568.8	14.8	730	12	BI601346	BI601346 603245090
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c 31	556.4	14.5	741	14	CB169095	CB169095 IMU602702
32	556.2	14.5	650	14	CB215381	CB215381 NISC_np05
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34	553	14.4	699	12	BG819566	BG819566 602783209
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37	552	14.4	817	14	CA322433	CA322433 UI-M-FX0-
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ALIGNMENTS

RESULT 1

AF125103

LOCUS AF125103 1798 bp mRNA linear HTC 22-MAY-2001

DEFINITION Homo sapiens neuroendocrine specific protein c homolog mRNA, complete cds.

ACCESSION AF125103

VERSION AF125103.1 GI:5107001

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1798)

AUTHORS Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G., Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W., Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
TITLE Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells

JOURNAL Genome Res. 10 (10), 1546-1560 (2000)

MEDLINE 20499367

PUBMED 11042152

REFERENCE 2 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Direct Submission

JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China

FEATURES Location/Qualifiers

source 1..1798

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_type="CD34+ hematopoietic stem/progenitor cells"

CDS 215..814

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BASE COUNT 540 a 314 c 392 g 552 t

ORIGIN

Query Match 25.7%; Score 986; DB 11; Length 1798;
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 Matches 1360; Conservative 0; Mismatches 140; Indels 80; Gaps 21;

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AF077050
LOCUS AF077050 1785 bp mRNA linear HTC 21-NOV-2002
DEFINITION Homo sapiens neuroendocrine-specific protein C homolog mRNA,
complete cds.
ACCESSION AF077050
VERSION AF077050.1 GI:4689147
KEYWORDS HTC..
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X.,
Luo,B., Hu,R. and Chen,J.
TITLE Human neuroendocrine-specific protein C (NSP) homolog gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1785)
AUTHORS Song,H.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of
Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,
Shanghai 200025, P.R. China
FEATURES
Location/Qualifiers
source 1. .1785
/organism="Homo sapiens"
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CDS 214. .813
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ORIGIN

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[illegible]

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JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
 Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
 Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
 Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
 Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
 Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
 Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
 Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
 Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3533)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3533
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9430059L06"
/db_xref="taxon:10090"
/clone="9430059L06"
/tissue_type="embryonic body between diaphragm region and
neck"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"

misc_feature 1. .3533
/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO
PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog
[Rattus norvegicus] (SWISSPROT|Q9JK11, evidence: FASTY,
95.8%ID, 100%length, match=1068)"

BASE COUNT 955 a 774 c 840 g 964 t

ORIGIN

Query Match 20.2%; Score 774.2; DB 11; Length 3533;
Best Local Similarity 78.3%; Pred. No. 5.1e-101;
Matches 1190; Conservative 0; Mismatches 258; Indels 71; Gaps 19;

Qy 2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db 740 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 799
|||||

Qy 2364 TTGTTCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
|| |||||

Db 800 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 859
|||||

Qy 2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
|||||

Db 860 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 919
|||||

Qy 2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
|||||

Db 920 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 979
|||||

Qy	2544	GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAAGTGCACAATAAAAA	2603
Db	980	GAGGAATTGGTTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAA	1039
Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	1040	GAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG	1099
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT	2723
Db	1100	ATGTGAGTATTTACTTACGTTGGTGCCTTGTTCATGGTTTGACACTACTGATTTTAGCT	1159
Qy	2724	CTGATTTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	1160	CTGATCTCACTCTTCAGTATTCTGTTATATATGAACGGCATCAGGCGCAGATAGATCAT	1219
Qy	2784	TATCTGGGACTTGCAAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	1220	TATCTAGGACTTGCAAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC	1279
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	1280	CCTGGATTGAAGCGCAAAGCAGAATGAAAAGGCCCAACAGTAGACA-----TTC	1330
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTG-GGGAGGGTCAGGGAAGAACAAAGCCT	2962
Db	1331	ATCTTTAAAGGGGACACTCCCTTGGTTACGGGTGGGCGGGTCAGGGGTGAGCCCTGGGT	1390
Qy	2963	TGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACGCAGTGTCTGAGGAAAAA	3022
Db	1391	GGCCGTGCAGTTTCAG-----TTATTTTATAGCAGTGCAGTGTGAGGAAAAA	1438
Qy	3023	TGACCTGTCTTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGA	3082
Db	1439	TTACCTGTCTTTGACT-TCCTGTGTTTATCATCTTAAGTATTGTAAGCTGCTGTGTATGGA	1497
Qy	3083	TTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATAAAACAAGATCT	3142
Db	1498	TCT-CATTGTAGTCATACTGTTTTCCCCAGATGAGGCACTTGGTGAATAAAGGATG-CT	1555
Qy	3143	GAGAAAGCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGTATTTGGGGAATTGCAAA	3202
Db	1556	GGGAAAACGTGTGTATTATATTCTGTTGCAGGTAGTCTGGCTGTATTTGGAAAGTTGCAAA	1615
Qy	3203	GAAAGTGGA----GCTGACAGAAATAACCCCTTTTCACAGTTTGTGCAGTGTGTACGGTCT	3258
Db	1616	GAAGGTAGATTTGGGGGCAGGAAAAACAACCCCTTTTCACAGTGTACTGTGTTTGGTTGGT	1675
Qy	3259	GTGTAGGTGTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACCAAGGC	3318
Db	1676	GTAAACTGATGCAGATTTTCTGAAATGAGATGTTTAGATGAG--CATACTACTAAAGC	1733
Qy	3319	AGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTG	3378
Db	1734	AGAGTGGAAAAATCTGTC--TTATGGTATGTTCTAGGTGTATTGTGATTTACTGT----	1787

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI051CA06NP1&cluster=1423.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI051CA06NP1.

FEATURES Location/Qualifiers
 source 1. .956
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI051YB11"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 283 a 219 c 207 g 237 t 10 others
ORIGIN

Query Match 17.4%; Score 668.6; DB 9; Length 956;
Best Local Similarity 88.7%; Pred. No. 8.5e-86;
Matches 795; Conservative 3; Mismatches 67; Indels 31; Gaps 6;

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Qy      2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db      878 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 819

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
          |||
Db      818 CTATTCCTGCTGCTTTTCATTRACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 759

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      758 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 699

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      698 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 639

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTGTAAGTGCACAATAAAA 2603
          |||
Db      638 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 579

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
          |||
Db      578 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 519

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      518 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 459

Qy      2724 CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          |||
Db      458 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 399

Qy      2784 TATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
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Db	398	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	339
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	338	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC	284
Qy	2904	ATCTTTAAAGGGGATATTCAATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT	2963
Db	283	ATCTTTAAAGGGGATATTCAATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTT	225
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTGTAGCAACGCAGTG-T	3011
Db	224	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCACTGTT	165
Qy	3012	CTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	164	GTGAGGAAAAATTACCTGTCTTTACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	105
Qy	3072	CTATGTATGGATTTAAATCGTAATCATATTTGTTTTCCTGTATGAGGCACCTGGTGAATA	3131
Db	104	CTATGTATGGATTTAAACCGYAATCATA--TCCTTTTCCTATCTGAGGCACCTGGTGA--	49
Qy	3132	AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT	3187
Db	48	-----ATAAAAAACCTGNANATTNNNACTTGTGCGAGATAGTCTGGCCGCMT	2

RESULT 5

CB204418

LOCUS CB204418 896 bp mRNA linear EST 05-FEB-2003

DEFINITION AGENCOURT 11276017 NIH MGC 135 Mus musculus cDNA clone

IMAGE:30138586 5', mRNA sequence.

ACCESSION CB204418

VERSION CB204418.1 GI:28241848

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 896)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM0041 row: k column: 11

High quality sequence stop: 686.

FEATURES	Location/Qualifiers
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source      1.  .896
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Qy	1389	TGTGATTTTAATTAAAGAAACAAAGATCTCTACTGACCGACTCCAGATTTCTCTAGTTAT	1448
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Qy	1449	TCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGATTCC	1508
Db	548	TCAGAAATGCGAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTAGTTGAAGATTCC	607
Qy	1509	TCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCACAA	1568
Db	608	TCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAA	667
Qy	1569	AAACAAGATGAAGCTGTAAATACTTGTGAAAGAAAACCTCACTGAAATTTTCATCTGAGTCA	1628
Db	668	AAACAAGATGAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACTTCATTTGAGTCA	727
Qy	1629	ATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAGGGAGGAAAA	1688
Db	728	ATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCG--CACCTGAGGGGNAGAAG	784
Qy	1689	CCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG-CACCTGA	1747
Db	785	NCATANTTGGAACTCTTTAAGCTCAGTTTAGATAACACNANAGATACCTGGTTACCTGA	844
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Db	845	TGAAGGTT	852

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FEATURES                      Location/Qualifiers
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                              /lab_host="DH10B"
                              /clone_lib="MARC 6BOV"
                              /note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
BASE COUNT      207 a      114 c      122 g      203 t
ORIGIN

Query Match          16.4%;  Score 628.8;  DB 14;  Length 646;
Best Local Similarity 99.4%;  Pred. No. 4.5e-80;
Matches 642;  Conservative 0;  Mismatches 2;  Indels 2;  Gaps 1;

Qy      3177 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTTCACA 3236
      |||
Db      1 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTTCACA 60

Qy      3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
      |||
Db      61 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 120

Qy      3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG 3356
      |||
Db      121 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG 180

Qy      3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATA 3414
      |||
Db      181 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 240

Qy      3415 TATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 3474
      |||
Db      241 TATCTATATATAGTGTTCATGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 300

Qy      3475 TTGATACTTCTGTGCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 3534
      |||
Db      301 TTGATACTTCTGTGCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 360

Qy      3535 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAACAGAAC 3594
      |||
Db      361 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAACAGAAC 420

Qy      3595 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAACACTCTGGA 3654
      |||
Db      421 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAACACTCTGGA 480

Qy      3655 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 3714
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Db      481 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 540

Qy      3715 AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATT 3774
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Db 541 AAATGACGATTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATT 600

Qy 3775 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAA 3820
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Db 601 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACCTAAAAA 646

RESULT 8

BM986175

LOCUS BM986175 627 bp mRNA linear EST 22-MAR-2002

DEFINITION LM24HW00149 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone
 LM-24-HW-001-49 (5'), mRNA sequence.

ACCESSION BM986175

VERSION BM986175.1 GI:19684841

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 627)

AUTHORS Yoon,D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R.,
 Sun,S.S. and Cheong,I.C.

TITLE Gene Expression Profiling of the Bovine skeletal muscle

JOURNAL Unpublished

COMMENT Contact: Dr. Du-Hak Yoon
 National Livestock Research Institute, RDA
 564 Omockchun-dong, Suwon, 441-350, Korea
 Tel: 82 31 290 1593
 Fax: 82 31 290 1792
 Email: dhyoon@rda.go.kr
 Insert Length: 839 Std Error: 0.00
 Seq primer: CAGGAAACAGCTATGAC
 POLYA=No.

FEATURES Location/Qualifiers

source 1. .627
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
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 /sex="six males mixed"
 /tissue_type="longissimus dorsi"
 /cell_type="myocyte"
 /dev_stage="24 months old"
 /lab_host="XL1-BlueMRF'strain"
 /clone_lib="Bos taurus LM-24-HW cDNA library"
 /note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1:
 EcoRI; Site_2: Xho I"

BASE COUNT 191 a 95 c 148 g 193 t

ORIGIN

Query Match 16.3%; Score 625.4; DB 12; Length 627;
 Best Local Similarity 99.8%; Pred. No. 1.4e-79;
 Matches 626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2766 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 2825
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Db          1 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 60
Qy          2826 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 2885
          |||
Db          61 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 120
Qy          2886 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 2945
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Db          121 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 180
Qy          2946 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTACAGATCTTTATTTTTAGCAACG 3005
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Db          181 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTACAGATCTTTATTTTTAGCAACG 240
Qy          3006 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGT 3065
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Db          241 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGT 300
Qy          3066 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 3125
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Db          301 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 360
Qy          3126 TGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGT 3185
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Db          361 TGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGT 420
Qy          3186 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCA 3245
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Db          421 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCA 480
Qy          3246 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 3305
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Db          481 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 540
Qy          3306 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCCTGGTATGTTCTAGGTGTATTGTG 3365
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Db          541 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCCTGGTATGTTCTAGGTGTATTGTG 600
Qy          3366 AAATTTACTGTTGTATTAATTGCCAAT 3392
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Db          601 AAAATTACTGTTGTATTAATTGCCAAT 627

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RESULT 9

BG570231

LOCUS BG570231 843 bp mRNA linear EST 10-APR-2001

DEFINITION 602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5', mRNA sequence.

ACCESSION BG570231

VERSION BG570231.1 GI:13577884

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1567 row: o column: 07
 High quality sequence stop: 801.

FEATURES Location/Qualifiers
 source 1. .843
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 /mol_type="mRNA"
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 /clone="IMAGE:4717662"
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 /clone_lib="NIH_MGC_77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

BASE COUNT 224 a 158 c 194 g 267 t
 ORIGIN

Query Match 16.2%; Score 621.4; DB 10; Length 843;
 Best Local Similarity 87.6%; Pred. No. 4.7e-79;
 Matches 742; Conservative 0; Mismatches 86; Indels 19; Gaps 5;

Qy 2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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 Db 2 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 61

Qy 2364 TTGTTCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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 Db 62 CTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 121

Qy 2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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 Db 122 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 181

Qy 2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
 |||
 Db 182 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 241

Qy 2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
 |||
 Db 242 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 301

Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG	2663
Db	302	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG	361
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	362	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	421
Qy	2724	CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	422	CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	481
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	482	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	541
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	542	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	596
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	597	ATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACAAGCCTT	656
Qy	2964	GACATTGCAGTGCAGTTTCACAGAT-----CTTTATTTTGTAGCAACGCAGTG-T	3011
Db	657	ACGTTTGCAGTGCAGTTTCACAGATCGTAGTAGATCCTTTATTTTGTAGCCCTGCAGTGT	716
Qy	3012	CTGAGGAAAAATGACCTGTCTTGAAGT-GCCCTGTGTTTCATCATCTTAA-GTATTGTAAGC	3069
Db	717	GTGCAGGAAAAATACCTGTCTTGAAGTGGCCATGTTGTTCATCATCTTAAAGTATTGTAAGC	776
Qy	3070	TGCTATGTATGGATTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAA	3129
Db	777	TGCTATGTATGGATTAAACCGTATCATATCTTTTCTATCTAATCTGAGGACTGTGGAA	836
Qy	3130	TAAACAA	3136
Db	837	TTAAAAA	843

RESULT 10

BF044381

LOCUS BF044381 631 bp mRNA linear EST 10-OCT-2000

DEFINITION BP250021B10D3 Soares normalized bovine placenta Bos taurus cDNA clone BP250021B10D3 5', mRNA sequence.

ACCESSION BF044381

VERSION BF044381.1 GI:10761508

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 631)

AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson

,J.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATACGACTCACTATAGGG
 BACKWARD: ATTAACCCTCACTAAAG
 Insert Length: 631 Std Error: 0.00
 Plate: BP250021B10 row: D column: 3
 Seq primer: AGCGGATAACAATTTACACAGGA
 High quality sequence stop: 631.

FEATURES Location/Qualifiers
 source 1. .631
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250021B10D3"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT 188 a 97 c 142 g 204 t
 ORIGIN

Query Match 16.1%; Score 617; DB 10; Length 631;
 Best Local Similarity 99.7%; Pred. No. 2.2e-78;
 Matches 629; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 2834 AGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 2893
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 Db 1 AGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 60
 Qy 2894 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 2953
 |||
 Db 61 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 120
 Qy 2954 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACGCAGTGTCT 3013
 |||
 Db 121 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACGCAGTGTCT 180

Qy 3014 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT 3073
 |||
 Db 181 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT 240

Qy 3074 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 3133
 |||
 Db 241 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 300

Qy 3134 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGCAGGTAGTCTTGCTGTATTTGGGG 3193
 |||
 Db 301 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGCAGGTAGTCTTGCTGTATTTGGGG 360

Qy 3194 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTTCACAGTTTGTGCACTGTGTAC 3253
 |||
 Db 361 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTTCACAGTTTGTGCACTGTGTAC 420

Qy 3254 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 3313
 |||
 Db 421 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 480

Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
 |||
 Db 481 AAGGCAGGAGTGAAAAAGCTTGCCTTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 540

Qy 3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATATATCTATATATAGTGTT 3431
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 Db 541 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATATCTATATATAGTGTT 600

Qy 3432 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 3462
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 Db 601 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 631

RESULT 11
 CB521332

LOCUS CB521332 822 bp mRNA linear EST 28-MAR-2003
 DEFINITION UI-M-GH0-cem-h-13-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
 IMAGE: 6841502 5', mRNA sequence.

ACCESSION CB521332
 VERSION CB521332.1 GI:29354687
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 822)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>

,J.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATACGACTCACTATAGGG
 BACKWARD: ATTAACCCTCACTAAAG
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 Seq primer: AGCGGATAACAATTTACACAGGA
 High quality sequence stop: 593.

FEATURES
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 1. .593
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250015A10C2"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT 167 a 100 c 136 g 190 t
 ORIGIN

Query Match 15.4%; Score 591.4; DB 10; Length 593;
 Best Local Similarity 99.8%; Pred. No. 9.8e-75;
 Matches 592; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2488 AATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGG 2547
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 Db 1 AATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGG 60
 Qy 2548 AGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAAC 2607
 |||
 Db 61 AGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAAC 120
 Qy 2608 TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT 2667
 |||
 Db 121 TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT 180

Qy 2668 GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA 2727
 |||
 Db 181 GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA 240
 Qy 2728 TTTCACCTCTTCAGTGTTCTGTATTATTTATGAACGGCATCAGGCGCAAATAGATCATTATC 2787
 |||
 Db 241 TTTCACCTCTTCAGTGTTCTGTATTATTTATGAACGGCATCAGGCGCAAATAGATCATTATC 300
 Qy 2788 TGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTG 2847
 |||
 Db 301 TGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTG 360
 Qy 2848 GATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCT 2907
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 Db 361 GATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCT 420
 Qy 2908 TTAAAGGGGATATTTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACA 2967
 |||
 Db 421 TTAAAGGGGATATTTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACA 480
 Qy 2968 TTGCAGTGCAGTTTCACAGATCTTTATTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACC 3027
 |||
 Db 481 TTGCAGTGCAGTTTCACAGATCTTTGTTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACC 540
 Qy 3028 TGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATG 3080
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 Db 541 TGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATG 593

RESULT 14

BI775114

LOCUS BI775114 587 bp mRNA linear EST 25-SEP-2001

DEFINITION 467491 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BI775114

VERSION BI775114.1 GI:15776091

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 587)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
 ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTTCCCAGTCACGACG
 Plate: 144 row: C column: 22
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9913"
	/tissue_type="pooled"
	/lab_host="DH10B"
	/clone_lib="MARC 1BOV"
	/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

BASE COUNT 166 a 103 c 134 g 184 t
 ORIGIN

Query Match 15.3%; Score 587; DB 12; Length 587;
 Best Local Similarity 100.0%; Pred. No. 4.2e-74;
 Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2469	GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	CAGGGCATATTTGGAATCT	2528
Db	1	GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	CAGGGCATATTTGGAATCT	60
Qy	2529	GAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGCAATTCTGCTCTTGGTCATGTT	2588
Db	61	GAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGCAATTCTGCTCTTGGTCATGTT	120
Qy	2589	AACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATT	TAGTTGATTCTCTG	2648
Db	121	AACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATT	TAGTTGATTCTCTG	180
Qy	2649	AAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	TCAATGGTCTGACA	2708
Db	181	AAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	TCAATGGTCTGACA	240
Qy	2709	CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTAT	TTTATGAACGGCATCAG	2768
Db	241	CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTAT	TTTATGAACGGCATCAG	300
Qy	2769	GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGAT	GCCTATGGCTAAA	2828
Db	301	GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGAT	GCCTATGGCTAAA	360
Qy	2829	ATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAA	GCCTGAAAAGAGTTA	2888
Db	361	ATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAA	GCCTGAAAAGAGTTA	420
Qy	2889	ACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCAT	TGGGGAGGGTCAGG	2948

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Db      421 ACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGG 480
Qy      2949 GAAGAACAAAGCCTTGACATTGCAGTGCAGTTTTCACAGATCTTTATTTTGTAGCAACGCAG 3008
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GAAGAACAAAGCCTTGACATTGCAGTGCAGTTTTCACAGATCTTTATTTTGTAGCAACGCAG 540
Qy      3009 TGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCT 3055
        ||||||||||||||||||||||||||||||||||||||||||
Db      541 TGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCT 587

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RESULT 15

BM801698

LOCUS BM801698 958 bp mRNA linear EST 05-MAR-2002

DEFINITION AGENCOURT_6458941 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5558493
5', mRNA sequence.

ACCESSION BM801698

VERSION BM801698.1 GI:19118521

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 958)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12281 row: i column: 22

High quality sequence start: 25

High quality sequence stop: 579.

FEATURES

source

Location/Qualifiers

1. .958

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5558493"

/tissue_type="duodenal adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_88"

/note="Organ: small intestine; Vector: pCMV-SPORT6;

Site_1: NotI; Site_2: SalI; Cloned unidirectionally;

oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 247 a 215 c 218 g 278 t

ORIGIN

Query Match

15.2%; Score 581.2; DB 12; Length 958;

Best Local Similarity 91.5%; Pred. No. 2.4e-73;
Matches 639; Conservative 0; Mismatches 53; Indels 6; Gaps 2;

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Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
          |
Db      126 CTATTCCCTGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 185

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Db      186 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 245

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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Db      246 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 305

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
          |||
Db      306 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 365

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
          |||
Db      366 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 425

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      426 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 485

Qy      2724 CTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
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Db      486 CTCATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 545

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      546 TATCTACGACTTGCAAATAAGAATGCTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 605

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
          |||
Db      606 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCAAAATAATTA-----GTACGAGTTC 660

Qy      2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT 2963
          |||
Db      661 CTCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAGGCAAGAACGAA-CCTT 719

Qy      2964 GACATTGCAGTGCAGTTTCACAGATCTTTATTTTAGC 3001
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Db      720 GACGTTGCAGTGCAGTTTCACAAATCGCTGGTTAGATC 757

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Job time : 7424.52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 00:42:43 ; Search time 918.523 Seconds
(without alignments)
11264.762 Million cell updates/sec

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Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	1	3833 100.0 3833	21	AAD01174	Bovine neurite gro
	2	2687.8 70.1 4822	24	ABS70449	Human bone remodel
	3	2649.8 69.1 4632	24	ABV94680	Human pancreatic c
	4	2566.4 67.0 4698	25	ABX34563	Human mddt cDNA SE
	5	2379.4 62.1 4053	22	AAS09453	Human cDNA encodin
	6	2370.4 61.8 4093	21	AAA23454	cDNA encoding huma
	7	2223.6 58.0CTG3579	21	AAZ56886	Human MAGI polypep
	8	2223.6 58.0 3579	22	AAF90324	Human NOGO-A cDNA.
	9	2223.6 58.0 3579	24	ABN86601	Human neurotransmi
	10	2223.6 58.0 3579	24	ABK90134	DNA encoding human
	11	2183.4 57.0 4684	21	AAD01173	Rat neurite growth
	12	2179.4 56.9 4684	24	ABN86600	Rat neurotransmitt
	13	1777.2 46.4 2386	19	AAV30920	Human secreted pro
	14	1774 46.3 2386	22	AAF98399	Human cDNA clone B
	15	1414.6 36.9 1980	22	AAI98079	Human neuroblastom
c	16	1039.8 27.1 1758	22	AAF32725	Human secreted pro
	17	1031.8 26.9 2240	21	AAC64406	Human Nogo B nucle
	18	1025.4 26.8 2235	24	ABV94681	Human pan704Y
	19	989.2 25.8 1514	24	ABK34580	Human cDNA for nov
	20	986 25.7 1798	24	ABK90135	DNA encoding human
	21	827.2 21.6 2052	24	ABK90133	DNA encoding human
	22	750.4 19.6 1568	21	AAD01175	Rat neurite growth
	23	685.8 17.9 1213	20	AAX04379	Human secreted pro
	24	685.8 17.9 1610	21	AAZ36230	cDNA encoding a bo
	25	681.4 17.8 991	20	AAX97587	Extended human sec
	26	681.2 17.8 1694	22	AAK94408	Human full-length
	27	590.8 15.4 799	19	AAV23695	Human NSPLP protei
	28	573.4 15.0 770	21	AAA72983	Human NSPH encodin
	29	573.4 15.0 1216	24	ABA05903	Human RTN4B encodi
	30	539 14.1 1683	22	AAD0	Human secreted pro
	31	538.8 14.1 868	21	AAZ56887	Human MAGI polypep
c	32	535 14.0 4710	22	AAL04697	Human reproductive
c	33	535 14.0 4710	23	ABL97604	Human testicular a
	34	527 13.7 600	22	AAF90323	Human NOGO-C cDNA.
	35	527 13.7 1122	21	AAZ56888	Human MAGI polypep
	36	527 13.7 1122	22	AAF90325	Human NOGO-B cDNA.
	37	464 12.1 472	25	ABX50578	Bovine EST associa
	38	463.4 12.1 3535	22	AAH72837	Human cervical can
	39	427.2 11.1 447	25	ABX50261	Bovine EST associa
	40	427 11.1 441	25	ABX53872	Bovine EST associa
	41	423.8 11.1 429	25	ABX53062	Bovine EST associa
	43	418.8 10.9 422	25	ABX46402	Bovine EST associa
c	44	413.2 10.8 742	22	AAI96236	Human neuroblastom
	45	398 10.4 406	25	ABX50364	Bovine EST associa

ALIGNMENTS

RESULT 1

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; ss.

XX

OS Bos sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CH1900XT

TTGTC

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -

XX

PS Claim 26; Fig 12; 122pp; English.

XX

CC The present sequence is a cDNA encoding bovine Nogo protein which is a
 CC potent neural cell growth inhibitor and is free of all central nervous
 CC system (CNS) myelin material with which it is natively associated. The
 CC present sequence was obtained from bovine spinal cord white matter cDNA
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory
 CC activity are used in the treatment of neoplastic disease of the CNS
 CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
 CC menagioma, neuroblastoma, retinoblastoma and degenerative nerve TG 2745e
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
 CC promote Nogo activity can be used to treat or prevent hyperproliferative
 CC or benign dysproliferative disorders e.g. psoriasis and tissue
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
 CC inhibit production of Nogo protein to induce regeneration of neurons or
 CC to promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 other;

Query Match 100.0%; Score 3833; DB 21; Length 3833;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Qy	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Qy	181	TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	181	TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTGGATTGCTGGAGGTAATATAGAGAGCAAA	540
		8 ID NOS:	
Db	481	AAAGATACTTACAAGCAAGATAGTGATGTTTGGATTGCTGGAGGTAATATAGAGAGCAAA	540
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660

QY	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAAC	TGAGAAATGTTTCA	720
Db	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAAC	TGAGAAATGTTTCA	720
QY	721	ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAATAAGACAGATG	AAAAAAG	780
Db	721	ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAATAAGACAGATG	AAAAAAG	780
QY	781	ATAGAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC		840
Db	781	ATAGAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC		840
QY	841	CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA		900
Db	841	CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA		900
QY	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTTTCAGG		960
Db	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTTTCAGG		960
QY	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA		1020
Db	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA		1020
QY	1021	TGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACAGCTTT		1080
Db	1021	TGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACAGCTTT		1080
QY	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTCATGG		1140
Db	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTCATGG		1140
QY	1141	AAGCACCATTAAATCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT		1200
Db	1141	AAGCACCATTAAATCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT		1200
QY	1201	CACCATTAGAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC		1260
Db	1201	CACCATTAGAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC		1260
QY	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG		1320
Db	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG		1320
QY	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT		1380
Db	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT		1380
QY	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT		1440
Db	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT		1440
QY	1441	CTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG		1500
Db	1441	CTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG		1500

Qy	1501	AAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Db	1501	AAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Qy	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Db	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Qy	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG	1680
Db	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG	1680
Qy	1681	GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740
Db	1681	GTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740
Qy	1741	CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Db	1741	CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Qy	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Db	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Qy	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Db	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Qy	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Db	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Qy	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGAT	2040
Db	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGAT	2040
Qy	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Db	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Qy	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG	2160
Db	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG	2160
Qy	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Db	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Qy	2221	CCGAGAGAAAACCTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Db	2221	CCGAGAGAAAACCTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Qy	2281	CAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Db	2281	CAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Qy	2341	CTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400

Db	2341	 CTGGAGTGGTGTGTTGGTGCCAGCTGTTCTCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400
Qy	2401	 TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Db	2401	 TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Qy	2461	 ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTGAGGGCATATT	2520
Db	2461	 ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTGAGGGCATATT	2520
Qy	2521	 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
Db	2521	 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
G	Qy	2581	CTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGAGCTAGCTAG 2640
Db	2581	 GTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTG	2640
Qy	2641	 ATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Db	2641	 ATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Qy	2701	 GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAAC	2760
Db	2701	 GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAAC	2760
Qy	2761	 GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTA	2820
Db	2761	 GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAA1CCTGCTA	2820
Qy	2821	 TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Db	2821	 TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Qy	2881	 AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Db	2881	 AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Qy	2941	 GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Db	2941	 GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Qy	3001	 CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Db	3001	 CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Qy	3061	 ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGC	3120
Db	3061	 ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGC	3120
Qy	3121	 ACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Db	3121	 ACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Qy	3181	 GCTGTATTTGGGGAATTGCAAAGAAAGTGAGCTGACAGAAATAACCCCTTTTCACAGTTT	3240

Db 3181 GCTGTATTTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTT 3240
 Qy 3241 GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG 3300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3241 GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG 3300
 Qy 3301 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTA 3360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3301 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTA 3360
 Qy 3361 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA 3420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3361 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA 3420
 Qy 3421 TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3421 TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
 Qy 3481 CTTCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3481 CTTCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
 Qy 3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
 Qy 3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
 Qy 3661 CTAADATCTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA1050X10 AATGA 3720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAAATATAAATGA 3720
 Qy 3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
 Qy 3781 TGTAAGCAAGTATCAATAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3781 TGTAAGCAAGTATCAATAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833

RESULT 2

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

XX

OS Homo sapiens.

XX

PN US6426186-B1.
XX
PD 30-JUL-2002.
XX
PF 18-JAN-2000; 2000US-0484970.
XX
PR 18-JAN-2000; 2000US-0484970.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2002-673014/72.
XX
PT A combination of polynucleotides which are co-expressed with genes
PT known to be involved in bone remodeling and osteoporosis are useful in
PT an array for the diagnosis of bone remodeling and osteoporosis
PT associated disorders -
XX
PS Claim 1; Column 283-288; 206pp; English.
XX
CC The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are
CC co-expressed with genes known to be involved in bone remodelling and
CC osteoporosis. The invention is used to diagnose disorders associated
CC with bone remodelling o orosis. ABS70344-ABS70512 represent |
CC human bone remodelling genes of the invention.
XX
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 15 other;

Query Match 70.1%; Score 2687.8; DB 24; Length 4822;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 3333; Conservative 0; Mismatches 458; Indels 104; Gaps 27;

Qy 1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
|| ||||||||||||||||||| ||| ||||||| ||||||||||||| ||| || ||
Db 964 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 1023

Qy 61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTTCTCA 120
||| | ||||||||||||||||||| || || | ||||||||||||| |||||
Db 1024 GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 1083

Qy 121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAATTTTTCAGAATTGGAATAT 180
||||||||||||||| || | | ||||| || ||||||||||| ||||||||||| |||||
Db 1084 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1143

Qy 181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
||||||||||| ||||| ||||||| ||||| || ||||||| ||||||||| |||||
Db 1144 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAGCAGAACTGCGGTAATAGTAGCA 1203

5

Qy 241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
||||||||||| ||||| | |||| | || ||||| ||||||| | ||||||| |
Db 1204 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1263

Qy 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
||||||||||| ||| || ||||| ||||| ||||| ||||| ||| ||||| ||
Db 1264 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1323

Qy	361	GATAGAGTTCGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTCAGCA	420
Db	1324	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1380
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGTGAGCGAGTATGGGAAGTG	480
Db	1381	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGTGAGCGAGTATGGGAAGTG	1440
Qy	481	AAAGATACTTACAAGCAAGATAGTGTATTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1441	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC	1497
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1458	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAAACAAATCACGAA	1557
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAAG	660
Db	1558	AAAGATAGTGAGAGTAGTAATGATGATAC'TTC'TTTCCCCAGTACGCCAGAAGGTATAAAG	1617
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCC--CAACAACTGAGAATGTT	717
Db	1618	GATCGTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1677
Qy	718	TCAACAAACATTTTTCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1678	GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1737
Qy	778	AAGA--TAGAAAAAAAAAGGCACAAATTGTAAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db	1738	AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC	1797
Qy	836	AAACCC-TTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATG	894
Db	1798	AAACCCTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATT	1857
Qy	895	TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGG	954
Db	1858	TAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAG	1917
Qy	955	TTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTCGCTTTGAAA	1014
Db	1918	TACAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAA	1977
Qy	1015	CAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAAC	1074
Db	1978	CAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCAC	2037
Qy	1075	AGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGGTTTTGCCTGACATTG	1134
Db	2038	AGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTG	2097
Qy	1135	TCATGGAAGCACCATTAATTTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCA	1194
Db	2098	TTATGGAAGCACCATTAATTTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCA	2157

Qy	1195	GTTCATCACCATTAGAAAACCTCTCCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTG	1254
Db	2158	GCTCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTG	2214
Qy	1255	AAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGA	1314
Db	2215	AAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAA	2274
Qy	1315	ATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTT	1374
Db	2275	AGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTT	2334
Qy	1375	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAG	1434
Db	2335	Homo sapieTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGG	2394
Qy	1435	ATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGC	1494
Db	2395	ATTTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCTGATCATTCTGAGC	2454
Qy	1495	TAGTTGAAGATTCTCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGTATGATTCAATAC	1554
Db	2455	TAGTTGAAGATTCTCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGTATGATTCAATAC	2514
Qy	1555	CCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAA	1614
Db	2515	CTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGA	2574
Qy	1615	TTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTTACCATCAC	1674
Db	2575	CTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCCTTTGC---CAC	2631
Qy	1675	CTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATA	1734
Db	2632	CTGAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATA	2691
Qy	1735	CCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAA TCCCTTTGCAGATGG	1794
Db	2692	CCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCCTTTGCAGATGG	2751
Qy	1795	AGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTATTGCTCAGGAAGCAAACC	1854
Db	2752	AGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGA	2811
Qy	1855	TAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGA	1914
Db	2812	TAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTA	2871
Qy	1915	CCTTTGTCAGTTCTAAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAACAGTTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAG	2931
Qy	1975	AAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTG	2034
Db	2932	AAGTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTTCATTGCCTTGCA	2991
Qy	2035	CAGGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088

Db	3832	TGAAAACGCCCAAAATAATTA-----GTAGGAGTTTCATCTTTAAAGGGGATATTCATTTG	3886
Qy	2928	ATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC---	2984
Db	3887	ATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGA	3945
Qy	2985	-----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTTGA	3035
Db	3946	TCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTTGA	4005
Qy	3036	CTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAAT	3095
Db	4006	CTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAAT	4065
Qy	3096	CATATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAGATCTGAGAAAGCTGTAT	3155
Db	4066	CATA--TCTTTTTCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTAT	4112
Qy	3156	ATTACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGAGCT	3214
Db	4113	ATTTTACTTTGTGTCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT	4172
Qy	3215	-----GACAGAAATAAACCTTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGT	3266
Db	4173	AGAAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGAT	4232
Qy	3267	TGATGCAGATTTTCTGAAATGAAA---TGTTTAGACGAGATCATGCCACCAAGGCAGGA	3322
Db	4233	TGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGA	4292
Qy	3323	GTGAAAAGCTTGCCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATT	3382
Db	4293	ATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATT	4351
Qy	3383	AATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTT	3442
Db	4352	AATTGCCAATATAAGTAAATATAGATTATATATG-----TATAGTGTTTCACAAAGCTT	4405
Qy	3443	AGCCCTTTACCTTCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTT	3496
Db	4406	AGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTACAGAGTCAGTCATTGGTTA	4464
Qy	3497	TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAAACGTACTTCTAGGCGCACTACCA	3556
Db	4465	TACATGTGTAGTTCCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA	4524
Qy	3557	TCTGTTTTCAACACGAACCGACGCCATGCAACAGAACTCC-TCAACATAAACTTCACTG	3615
Db	4525	TCTGTTTTCAACATGAA--ATGCCACACACATAGAACTCCAACAACATCAATTTCAATTG	4581
Qy	3616	CACAGACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAA	3673
Db	4582	CACAGACTGACTGTAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAA	4641
Qy	3674	AAA-----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAAT	3718
Db	4642	AAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTATGCAAGAAATATTAATTTACAAAAT	4701

Qy 3719 GACGATTTATACAATTGTGGTTTAAGCTGTATTGAACATAAATCTGTGGAATGCATTGTGA 3778
||| ||||||||| ||||||||||||||||| ||| ||||||||||||||||| |||
Db 4702 GAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACATAAATCTGTGGAATGCATTGTGA 4761

Qy 3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
||| ||||||||||||||||||||| | |||
Db 4762 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAANGNNANNAGNGAAA 4816

RESULT 3

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX

AC ABV94680;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW cytostatic; tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX

PD 08-AUG-2002.

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PF 30-JAN-2002; 2002WO-US02A

XX

PR 30-JAN-2001; 2001US-265305P.

PR 31-JAN-2001; 2001US-265682P.

PR 09-FEB-2001; 2001US-267568P.

PR 21-MAR-2001; 2001US-278651P.

PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.

PR 12-JUL-2001; 2001US-305484P.

PR 20-AUG-2001; 2001US-313999P.

PR 27-NOV-2001; 2001US-333626P.

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PA (CORI-) CORIXA CORP.

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PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

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DR WPI; 2002-627435/67.

DR P-PSDB; ABP68600.

XX

PT New isolated polynucleotide and pancreatic tumor polypeptides, useful

PT for diagnosing, preventing and/or treating cancer, particularly

PT pancreatic cancer -

XX

PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising: (a)

CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99445);

CC (b) complements of (a); (c) sequences consisting of at least 20

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAAACAAACAAATCGTGAA	600
Db	1387	TTGGAAGGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACCTAATCACGAA	1446
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1447	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1506
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT	717
Db	1507	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1566
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA	777
Db	1567	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1626
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1627	AAAATAGAAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1686
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTCAACAGATCATGTG	896
Db	1687	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1746
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1747	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1806
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1807	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1866
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACAG	1076
Db	1867	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1926
Qy	1077	CTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1927	CTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1986
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1987	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2046
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
		- -	
Db	2047	TCATCACCATTAGAAGC--TTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA	2103
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2104	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2163
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376
Db	2164	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2223

Qy	1377	ATATCTATTGCGATGTGATTTTAATTAAAGAAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2224	ATATCTATTGCGATGTGATTTTAATTAAAGAAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2283
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTTCTGAGCTA	1496
Db	2284	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTTCTGAGCTA	2343
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2344	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2403
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2463
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTTACCATCACCT	1676
Db	2464	TCATTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACTCAGTGCCTTGC---CACCT	2520
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2580
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2640
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2641	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2700
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAAATTGAAATTATAGATGAGTTCCCTACA	2760
Qy	1917	TTTGTCACTTCTAAAGCAGATTCTTCTCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2820
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCA	2036
Db	2821	GTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCAATGCCTTGCA	2880
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAAACAGT	2940
Qy	2091	GTCCCGAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2941	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATGCTTCCA	3000
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3060
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	3061		GTGAAAGAAGCTGAGAAAAA	CTTCCTTCCGATA	CAGAAAAAGAGGACAGATCACCATCT	3120
Qy	2271		GCTATATTTTCAGCAGAGCTGAGTAA	AACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC		2330
Db	3121		GCTATATTTTCAGCAGAGCTGAGTAA	AACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC		3180
Qy	2331		ATTAAGAAGACTGGAGTGGTGT	TTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA		2390
Db	3181		ATTAAGAAGACTGGAGTGGTGT	TTGGTGCCAGCCTATTCCCTGCTGCTTTCATTGACAGTA		3240
Qy	2391		TTCAGCATTGTGAGTGTAACGGCCTACAT	TGCCCTTGGCCCTGCTCTCTGTGACTATCAGC		2450
Db	3241		TTCAGCATTGTGAGCGTAACAGCCTACAT	TGCCCTTGGCCCTGCTCTCTGTGACCATCAGC		3300
Qy	2451		TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC			2510
Db	3301		TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC			3360
Qy	2511		AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGCAAT		2570
Db	3361		AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGTAAT		3420
Qy	2571		TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT			2630
Db	3421		TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT			3480
Qy	2631		GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC			2690
Db	3481		GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC			3540
Qy	2691		TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT			2750
Db	3541		TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT			3600
Qy	2751		ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT			2810
Db	3601		ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT			3660
Qy	2811		AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA			2870
Db	3661		AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA			3720
Qy	2871		GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT			2930
Db	3721		AAACGCCCAAATAATTAGT-----AGGAGTTCATCTTTAAAGGGGATATTCATTTGATT			3775
Qy	2931		CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCT			2990
Db	3776		AT-----ACGGATCT			3785
Qy	2991		TTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCA			3049
Db	3786		TTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCA			3845
Qy	3050		TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTTTTC			3109

Db	3846	TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATA--TCTTTTTC	3903
Qy	3110	CTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCG	3169
Db	3904	CTATCTGAGGCACTGGTGGA-----ATAAAAACCTGTATATTTTACTTTGTGTTG	3952
Qy	3170	CAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAA	3222
Db	3953	CAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAA	4012
Qy	3223	TAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTG	3282
Db	4013	AAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTG	4072
Qy	3283	AAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCT	3338
Db	4073	AAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CT	4131
Qy	3339	TTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATGCCAATATAAGT	3398
Db	4132	TTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGT	4191
Qy	3399	AAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCC	3458
Db	4192	AAATATAGATTATATATG-----TATAGTGTTCACAAAGCTTAGACCTTTACCTT-CC	4244
Qy	3459	AGCTGCCCCACAGTGCTTGATACT-----TCTGTGTCATGGGTTTTATGTGTGTAGTCCCA	3512
Db	4245	AGCCACCCACAGTGCTTGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCA	4304
Qy	3513	AAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGA	3572
Db	4305	AAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGA	4364
Qy	3573	ACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAG	3631
Db	4365	A---ATGCCACACACATAGAACTCCAACAACATCAATTTTCATTGCACAGACTGACTGTAG	4421
Qy	3632	TTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGTTTG	3682
Db	4422	TTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTG	4481
Qy	3683	CAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTTTATACAATT	3734
Db	4482	CAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATT	4541
Qy	3735	GTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	3794
Db	4542	GTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	4601
Qy	3795	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA 3825	
Db	4602	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA 4632	

ID ABX34563 standard; cDNA; 4698 BP.
XX
AC ABX34563;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human mddt cDNA SEQ ID 124.
XX
KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US09944.
XX
PR 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR P-PSDB; ABU11573.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis -
XX
PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides

CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC o.int/pub/published_pct_sequences.

XX

SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 other;

Query Match 67.0%; Score 2566.4; DB 25; Length 4698;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 441; Indels 140; Gaps 25;

```
Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || |||||
Db      856 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 915

Qy     61 GTACTGCCCCACTGAAGGAACACTTCCAG-CAACTTCAAATGAAGCTTCTAAAGCATTCTC 119
      ||| | |||||
Db     916 GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTC 975

Qy    120 AGAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAAACAGAATTTTCAGAATTGGAATA 179
      |||||
Db    976 AGAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAAACAGAGTTTTCAGAATTAGAATA 1035

Qy    180 TTCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGC 239
      |||||
Db   1036 CTCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGC 1095

Qy    240 GAATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCT 299
      |||||
Db   1096 AAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAA 1155

Qy    300 TAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGA 359
      |||||
Db   1156 TAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGA 1215

Qy    360 AGATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGC 419
      ||  TGTG47$X || |||
Db   1216 TGA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGT 1272

Qy    420 AGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 479
      |||||
Db   1273 GGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 1332

Qy    480 GAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAA 539
      |||||
Db   1333 GAAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAA 1389

Qy    540 ATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGA 599
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Db	1390	CTTGGAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGA	1449
Qy	600	AAAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAG	659
Db	1450	AAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAA	1509
Qy	660	AGGTGGTTCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGT	716
Db	1510	GGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCAT	1569
Qy	717	TTCAACAAACATTTTTCCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAA	776
Db	1570	TGCAACAAACATTTTTCTTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAA	1629
Qy	4377	-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db	1630	AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC	1689
Qy	836	AAACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGT	895
Db	1690	AAACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTT	1749
Qy	896	GTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTGGT	955
Db	1750	AACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGT	1809
Qy	956	TCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAAC	1015
Db	1810	ACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTA GAAAC	1869
Qy	1016	AAAAATGGACCTGGTTCAAAC TTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACA	1075
Db	1870	AAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACA	1929
Qy	1076	GCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTGCCTGACATTGT	1135
Db	1930	GCTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGT	1989
Qy	1136	CATGGAAGCACCATTAAATTCGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAG	1195
Db	1990	TATGGAAGCACCATTGAATTCGTAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAG	2049
Qy	1196	TTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTGA	1255
Db	2056	ATTATGAAAGCATAAAACATGAGCCTGA	2106
Qy	1256	AAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAA	1315
Db	2107	AAATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAA	2166
Qy	1316	TGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTA	1375
Db	2167	GGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTA	2226
Qy	1376	TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGA	1435

Db	2227	TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGA	2286
Qy	1436	TTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCT	1495
Db	2287	TTTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCT	2346
Qy	1496	AGTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC	1555
Db	2347	AGTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC	2406
Qy	1556	CGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAAT	1615
Db	2407	TGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGAC	2466
Qy	1616	TTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACC	1675
		b4\$47\$Xt	
Db	2467	TTCATTTGAGTCAATGATAGAATATGAAAAAAGGAAAAACTCAGTGCTTTTGC---CACC	2523
Qy	1676	TGAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAC	1735
Db	2524	TGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAC	2583
Qy	1736	CTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGA	1795
Db	2584	CCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGA	2643
Qy	1796	GGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCT	1855
Db	2644	GGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGAT	2703
Qy	1856	AAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATT TAGATGAGTTCCCGAC	1915
Db	2704	AAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTAC	2763
Qy	1916	CTTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGA	1975
Db	2764	ATTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGA	2823
Qy	1976	AGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGC	2035
Db	2824	AGTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCATTGCCTTGCAC	2883
Qy	2036	AGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCA	2089
Db	2884	AGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAG	2943
Qy	2090	TGTCCCAGAT	
Db	2944	TTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCC	3003
Qy	2150	AGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCT	2209
Db	3004	AGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCT	3063
Qy	2210	TGTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATC	2269
Db	3064	TGTGAAAGAAGCTGAGAAAAAATTCCTTCCGATACAGAAAAAGAGGACAGATCACCATC	3123

Qy	2270	TGCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGA	2329
Db	3124	TGCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGA	3183
Qy	2330	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGT	2389
Db	3184	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGT	3243
Qy	2390	ATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAG	2449
Db	3244	ATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAG	3303
Qy	2450	CTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	2509
Db	3304	TATCTAGGACTACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATT	3363
Qy	2510	CAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAA	2569
Db	3364	CAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAA	3423
Qy	2570	TTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGA	2629
Db	3424	TTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGA	3483
Qy	2630	TGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGC	2689
Db	3484	TGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGC	3543
Qy	2690	CTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGT	2749
Db	3544	CTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGT	3603
Qy	2750	TATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGT	2809
Db	3604	TATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGT	3663
Qy	2810	TAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATG	2869
Db	3664	TAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAGCTGAATG	3723
Qy	2870	AGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGAT	2929
Db	3724	AAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGA-	3777
Qy	2930	TCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATC	2989
		60/03 6215X:	
Db	3778	-----TTATACGGATC	3788
Qy	2990	TTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTC	3048
Db	3789	TTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATACCTGTCTTGACTGCCATGTGTTTC	3848
Qy	3049	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTT	3108
Db	3849	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATA--TCTTTTT	3906

Qy	3109	CCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTTGTC	3168
Db	3907	CCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATTTTACTTTGT	3955
Qy	3169	GCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAG	3219
Db	3956	GCAGATAGTCTTGCCGCATCTTGCCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAG	4015
Qy	3220	AAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTT	3279
Db	4016	AAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTT	4075
Qy	3280	CTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTG	3335
Db	50X 6	CTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG	4135
Qy	3336	CCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATA	3395
Db	4136	-CTTTCCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATA	4194
Qy	3396	AGTAAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTT	3455
Db	4195	AGTAAATATAGATTATA-----TATGTATAGTGTTCACAAAGCTTAGACCTTTACCTT	4248
Qy	3456	CCCAGCTGCCCCACAGTGCTTGATACT-----TCGTGCATGGGTTTTATGTGTGTAGTC	3509
Db	4249	-CCAGCCACCCACAGTGCTTGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTT	4307
Qy	3510	CCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACA	3569
		/0	
Db	4308	CCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACA	4367
Qy	3570	CGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTG	3628
Db	4368	TGAA---ATGCCACACACATAGAAGCTCCAACAACATCAATTTTCATTGCACAGACTGACTG	4424
Qy	3629	TAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGT	3679
Db	4425	TAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGT	4484
Qy	3680	TTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTTATACA	3731
Db	4485	TTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACC	4544
Qy	3732	ATTGTGGTTTTAAGCTGTATTGA	3753
D	5	ATGGTAGCTTAAGCTGTACTGA	4566

RESULT 5

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease; AB020693; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT CDS 135..3713
FT /*tag= a
FT /product= "Nogo protein"

XX

PN WO200151520-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US01041 2

XX

PR 12-JAN-2000; 2000US-0175707.
PR 26-MAY-2000; 2000US-0207366.
PR 29-SEP-2000; 2000US-0236378.

XX

PA (UYYA) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2001-442138/47.
DR P-PSDB; AAU09453.

XX

PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders -

XX

PS Example 1; Page 95-100; 109pp; English.

XX

CC The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC relates to the use of the nogo receptor, nogo protein, their nucleic
CC acids, vectors expressing them and antibodies against them, to isolate
CC agents which block nogo receptor mediated axonal growth. The agent is
CC useful for treating a central nervous system disorder which is a result
CC of cranial or cerebral trauma, spinal cord injury, stroke or a
CC demyelinating disease selected from multiple sclerosis, monophasis
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC viral infection and Krabbe's disease.

XX

SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 other;

Query Match 62.1%; Score 2379.4; DB 22; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy     61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| || ||| | ||||| ||||| ||||| |||||
Db    906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCTAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy    121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Db    966 GAGADGCEAAATACTCTACTCATAGATAGAGATTTAACAGAGTTTT          AATAC 1025

Qy    181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1026 TCAGAAATGGGATCATCGTTCTAGTGTCTCTCAAAAGCAGAAATCTGCCGTAATAGTAGCA 1085

Qy    241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| || ||| || ||||| ||||| ||||| ||||| |||||
Db   1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy    301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy    361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1206 GAG-DAGTGTGTCTTCAG          AAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1262

Qy    421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1263 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1322

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| || ||| ||||| ||||| || ||| ||||| ||||| ||||| |||||
Db   1323 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1379

Qy    541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
Db   1380 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAACACGAA 1439

Qy    601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| || ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      0 AAAGATACTGAGAGTGTAGTAATGATGATACCTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1499

Qy    661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT 717
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1500 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1559

Qy    718 TCAACAAACATTTTTCCCTTGTTGGAAGATCACTTCCGAAAAATAAGACAGATGAAAAA 777
      ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db   1560 GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1619

Qy    778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
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Db	2457	TCATTTGAGTCAATGATAGAAATATGAAAAAAGGAAAAAATCAGTGCTTTGCG	2513
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAACC	1736
Db	2514	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTTGCGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATCCCTTTTGCGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAAAGTATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2814	GTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2874	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGADACGAGCTGCGCAAAAACCTTGGTGCCGATCTCTGAGGAGGAGGATCTCCATCT	3113
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGA	
Db	3174	ATTAAGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353

Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	353		
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGGAGCTATGGCTAAATTCAGGCAATGATCTTGAATGAAGCTGAGCTGAATGA	2890
Db	3654	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3714	AAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3768
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3769	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTGCAGTGCAGTTTCACAGATCG	3827
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3828	TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3887
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCAT	3098
Db	3888	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCAT	3947
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3948	A--TCTTTTTCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATT	3994
Qy	3159	ACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAGAAAGTGGAGCT	3214
Db	3995	TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT	4051

RESULT 6

AAA23454

ID AAA23454 standard; cDNA; 4093 BP.

XX

AC AAA23454;

XX

DT 19-JUN-2000 (first entry)

XX
DE cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1048..3729
FT /*tag= a
FT /product= "Human secreted protein vb22_1"
FT CDS 152..1006
FT /*tag= b
FT /product= "Clone vb22_1 ORF2"
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US19351.
XX
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099610X
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
DR P-PSDB; AAY95012, AAY95030.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 72; Page 321-322; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC in5XA on may exhibit 475XHe or more activities selected from the following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy

CC regime. Diseases or conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections, especially HIV; multiple sclerosis;
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
 CC insulin dependent diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. The present sequence represents cDNA
 CC encoding one of the 40 proteins of the invention.

XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 other;

Query Match 61.8%; Score 2370.4; DB 21; Length 4093;
 Best Local Similarity 86.4%; Pred. No. 0;
 Matches 2807; Conservative 0; Mismatches 386; Indels 55; Gaps 15;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA	60
Db	863	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	922
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	923	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	982
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAAATTGGAATAT	180
Db	983	GAGAAGGC-AAAACCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC	1041
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1042	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1101
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1102	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1161
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1162	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1221
Qy	361	GATGAGGCTC*1936Y1 39 AAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1222	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1278
Qy	421	GAAGCTTCTATGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1279	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1338
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1339	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1395

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1396	TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAA	1455
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1456	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1515
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1516	GATCGTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1575
Qy	718	TCAACAAACATTTTTCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1576	GCAACAAACATTTTTCCTTTGTTAGGAGATCTTACTTCAGAAAATAAGACCGATGAAAAA	1635
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1636	AAAATAGAAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1695
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1696	AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1755
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTT	956
Db	1756	ACAAAGGTGACTGAGGAAGTCTGTTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAGTA	1815
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1816	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1875
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAACACAG	1076
Db	1876	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1935
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTGCCTGACATTGTC	1136
Db	1936	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT	1995
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1996	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGC	2055
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2056	TCATCACCATTAGAAGCTT---CTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA	2112
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2113	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2172
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT	1376
Db	2173	GAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2232
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1433

Db	2233	 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2292
Qy	1437	 TTCTCTAGTTATTTCAGAAATAGCAGAAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2293	 TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2352
Qy	1497	 GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2353	 GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2412
Qy	1557	 GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2413	 GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2472
Qy	1617	 TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2473	 TCATTTGAGTCAATGATAGAATATGAAAAAAGGAAAAAACTCAGTGCTTTGC---CACCT	2529
Qy	1677	 GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2530	 GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2589
Qy	1737	 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2590	 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCCTTTGCAGATGGAG	2649
Qy	1797	 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2650	 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2709
Qy	1857	 AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2710	 AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2769
Qy	1917	 TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2770	 TTGATCAGTTCTAAAACGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2829
Qy	1977	 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2830	 GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACACA	2889
Qy	2037	 GGATTGCCCATGACCTTTCTTTCAAGAGTATACAAACCTA-----AAGAGGAAGTTCAT	2090
Db	2890	 GAATTGCCCATGACCTTTCTTTGAAGAACATACAAACCCAAAGTTGAAGAGAAAATCAGT	2949
Qy	2091	 GTCCAGATGAGTTCTCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2950	 TTCTCAGATGACTTTTCTAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	3009
Qy	2151	 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3010	 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3069
Qy	2211	 GTGAAAGAAGCCGAGAGAAAACCTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Accession	Position	Sequence	Position
Db	3070	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3129
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3130	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3189
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3190	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3249
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3250	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3309
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3310	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3369
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3370	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3429
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3430	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3489
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3490	GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3549
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3550	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3609
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3610	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3669
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3670	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3729
Qy	2871	GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTGATT	2930
Db	3730	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTGATT	3784
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3785	ATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACCTGTCAGTGCAGTTTCACAGATCG	3843
Qy	2985	-----AGATCTTTATTTTATAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3844	TTGTTAGATCTTTATTTTATAGCCATGCACCTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3903
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3904	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3963

XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleotide is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents a DNA encoding the human MAGI protein.
 XX
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 58.0%; Score 2223.6; DB 21; Length 3579;
 Best Local Similarity 87.5%; Pred. No. 0;
 Matches 2519; Conservative 6000 Mis55X: 339; Indels 22; Gaps 7;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAATTGGAATAT	180
Db	832	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCA DATE: GATCATCGTTCAGTGTCTCTCCAAAAGCAGAACTGCGGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
		475	
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305

Qy 601 AAAGATAGTGAAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
 |||||
 Db 1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1365

Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT 717
 |||||
 Db 1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1425

Qy 718 TCAACAAACATTTTTCCTTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA 777
 |||||
 Db 1426 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1485

Qy 778 AAGATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
 |||||
 Db 1486 AAGATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 1545

Qy 837 AACCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
 |||||
 Db 1546 AACCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 1605

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 956
 |||||
 Db 1606 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 1665

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA 1016
 |||||
 Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAGATTGCTTATGAAACA 1725

Qy 1017 AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACAG 1076
 |||||
 Db 1726 AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACAG 1785

Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTC 1136
 |||||
 Db 1786 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTC 1845

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
 |||||
 Db 1846 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGC 1905

Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
 |||||
 Db 1906 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1962

Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
 |||||
 Db 1963 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATGAAT 2022

Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT 1376
 |||||
 Db 2023 GAAGAAATTAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT 2082

Qy 1377 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 1436
 |||||
 Db 2083 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGAT 2142

Qy 1437 TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCAGCATTCTGAGCTA 1496

Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1650	GAGGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGA CTACA	2619
Qy	1917	TTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCT AAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330

Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTA	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCCTGCTGCTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 8

AAF90324

ID AAF90324 standard; cDNA; 3579 BP.

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AC AAF90324;

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DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A cDNA.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury;
 KW brain injury; stroke; neuronal degeneration; Alzheimer's disease;
 KW Parkinson's disease; neuromuscular disorder; psychiatric disorder;
 KW developmental disorder; neuroprotective; nootropic; neuroleptic;
 KW antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
 KW therapy; ss.

XX

OS Homo sapiens.

Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA--AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT--AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTTCAGATAGCCTTGAAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC--CAACAAGTGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTCTTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTCTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725

Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TC TAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916

Source	Accession	Sequence	Position
Db	2560	AGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTC	2036
Db	2680	GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGAC	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	209	AAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTACGTCAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTACGTCAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTG* CGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTTTTATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGT 50XT GAGGAGTTGGTTTCAGAAGTACAGCAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750

Db 3400 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT 3459

Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
 |||

Db 3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519

Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
 |||

Db 3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

RESULT 9

ABN86601

ID ABN86601 standard; DNA; 3579 BP.

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AC ABN86601;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; gene; ds.

XX

OS Homo sapiens.

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FH Key Location/Qualifiers

FT CDS 1..3579

FT /*tag= a

FT /product= "Nogo"

FT /note= "Nogo-A, Nogo-B and Nogo-C"

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PN US2002072493-A1.

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PD 13-JUN-2002.

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PF 28-JUN-2001; 2001US-0893348.

XX

PR 19-MAY-1998; 98IL-0124500.

PR 21-JUL-1998; 98WO-US14715.

PR 22-DEC-1998; 98US-0218277.

PR 19-MAY-1999; 99US-0314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR P-PSDB; ABB81078, ABB81079, ABB81080.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises

PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
XX
PS Disclosure; Page 49-53; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin - and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g. alcohol, organophosphates) No Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 58.0%; Score 2223.6; DB 24; Length 3579;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	61	GTA CTGCCC ACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAATTGGAATAT	180
Db	832	GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	181	TCAGAAATGGAATCATCATTCAAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGCA	951

Qy	241	AATCCTAGGGACGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAAACGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAATAAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCCTTTGTTAGGAGATCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTTCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1133

Db	1786	 CTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	 TCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1300	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	 GAAGAAATTAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTAAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	 ATATCTATTGCATGTGATTAAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	 TTCTCTAGTTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	 GTTGAAGATTCCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	 TCATTTGAGTCAATGATAGAAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	 GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	 GAGCTCAGTACTGCAGTTTATTCAAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCACTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	 AGAGAAACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
		 TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	

Db	2620	TTGATCAGTTCTAAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCT	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCT	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519

Qy 2811 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3520 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

RESULT 10

ABK90134

ID ABK90134 standard; DNA; 3579 BP.

XX

AC ABK90134;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis; gene; ds.

XX

OS Homo sapiens.

XX

FH	Key 50X	Location/Qualifiers	
FT	CDS	1..3579	
FT		/*tag= a	
FT		/product= "Human NogoA protein"	

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB00228.

XX

PR 18-JAN-2001; 2001GB-0001312.

XX

PA (GLAX) GLAXO GROUP LTD.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR P-PSDB; ABG30938.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides

PT -

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PS Disclosure; Page 53-58; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent

Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
 ||||| | | ||| ||||| ||| ||| ||||| ||| |||||
 Db 1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC 1245

Qy 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
 ||||| ||||| ||||| ||| ||| ||||| ||||| ||||| |||||
 Db 1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA 1305

Qy 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
 ||||| ||||| ||| ||||| ||||| ||||| ||| ||||| ||||| |||
 Db 1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCAGTACGCCAGAAGGTATAAAG 1365

Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT 717
 ||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||
 Db 1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1425

Qy 718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA 777
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1426 GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1485

Qy 778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAAATGCAAGTGTCAAGACATCA 836
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1486 AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAAATACTAGCACCAAAACATCA 1545

Qy 837 AACCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1546 AACCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA 1605

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTT 956
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1606 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAGTA 1665

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA 1016
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1725

Qy 1017 AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG 1076
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1726 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 1785

Qy 1077 CTTTGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTC 1136
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1786 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT 1845

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1846 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC 1905

Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1906 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA 1962

Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1963 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG 2022

Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT 1376

Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCTTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCCTT	2210

Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
0XG			
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTCACAGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTT	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 11

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

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AC AAD01173;

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DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

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KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 253..3744

FT /*tag= a

FT /product= "Nogo A"

FT /transl_except= (pos:1462..1464, aa:Ile)

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

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PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

DR P-PSDB; AAY71310.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

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PS Claim 26; Fig 2A; 122pp; English.

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CC The present sequence is a cDNA encoding rat Nogo A protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated.
CC The present sequence was generated by fusing R018U37-3, R1-3U21 cDNA
CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
CC library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for

Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTCCCTTGTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAA	1674
Qy	781	ATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCCTGTAACACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTCATG	1139
Db	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGTGCTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGTCTTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAAC	2151
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTTCTGAGCTAGTT	1499
Db	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Qy	1500	GAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559

Db 2389 GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAA 2448
 Qy 1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA 1619
 || ||||| ||||| || ||||| || || ||||| || || ||||| || ||
 Db 2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC- 2507
 Qy 1620 TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG 1679
 | || || || |||| |||| || || |||| |||| || || ||||
 Db 2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCCTCAC---CTCAGGAG 2559
 Qy 1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA 1739
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T 2616
 Qy 1740 GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG 1799
 ||| || |||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2617 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG 2676
 Qy 1800 CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTAAGA 1859
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2677 TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA 2736
 Qy 1860 GAAAGTGAAACATTTTCAGATTCTCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT 1919
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2737 GAAAGTGAAACATTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTT 2796
 Qy 1920 GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA 1979
 ||||| |||| | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2797 GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA 2853
 Qy 1980 GCCCACAAAAGTGAAATTGCTGACATCCAGGATG
 || ||||| ||||| || |||| | ||||| |||| | ||||
 Db 2854 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAA 2913
 Qy 2040 TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTTATGTCCCAGAT 2099
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2914 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT 2973
 Qy 2100 GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTACTGCCTCCAGATGTTTCT 2159
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
 Db 2974 GAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTCTCT 3033
 Qy 2160 GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA 2219
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 Db 3034 GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA 3093
 Qy 2220 GCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT 2279
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 Db 3094 GCAGAGAAAAAATTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG 3153
 Qy 2280 TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG 2339
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 5Db 8863154 ~~GGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG~~ 2039
 Qy 2340 ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT 2399
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3214 ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGCATT 3273

Qy 2400 GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA 2459
 || |||||
 Db 3274 GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA 3333

Qy 2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT CAGGGCATAT 2519
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 || |||||
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Qy 2580 GGT CATGT TAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 2639
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 Db 3454 GGT CATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513

Qy 2640 GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT 2699
 |||||
 Db 3514 GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573

Qy 2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAA 2759
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 Db 3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA 3633

Qy 2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 2819
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 Db 3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693

Qy 2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG 2879
 ||||| a |||ps 14;
 Db 3694 ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC 3753

Qy 2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTGATTCCATTGGGG 2939
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 Db 3754 AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC---GGG 3797

Qy 2940 AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTT 2999
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 Db 3798 GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTT 3855

Qy 3000 GCAACGCAGTGCTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG 3059
 ||| ||| |||||
 Db 3856 GCAGTGCAGTGTGTTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG 3914

Qy 3060 TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG 3119
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 Db 3915 TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGCTCTCCCAATGAGGC 3973

Qy 3120 CACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT 3179
 |||||
 Db 3974 GCCTGGTGAATAAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031

Qy 3180 TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT--GACAGAAATAACCCTTTTCACA 3236
 |||||
 Db 4032 AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCTTTTCACA 4091

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; gene; ds.
 XX
 OS Rattus norvegicus.
 XX
 FH Key Location/Qualifiers
 FT CDS 253..3744
 FT /*tag= a
 FT /product= "Nogo-A"
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-0893348.
 XX
 PR 19-MAY-1998; 98IL-0124500.
 PR 21-JUL-1998; 98WO-US14715.
 PR 22-DEC-1998; 98US-0218277.
 PR 19-MAY-1999; 99US-0314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR P-PSDB; ABB81074, ABB81076, ABB81077.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides -
 XX
 PS Disclosure; Page 40-44; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute

CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents a DNA
 CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
 CC and Nogo-C), an example of NS-specific antigen.

XX

SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 other;

Query Match 56.9%; Score 2179.4; DB 24; Length 4684;
 Best Local Similarity 78.2%; Pred. No. 0;
 Matches 3008; Conservative 0; Mismatches 731; Indels 110; Gaps 28;

Qy	1	CTATCTCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
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Qy	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT	1224
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA	1266
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1267	GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA	1326
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1327	GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG	1386
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1387	AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT-----	1434
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1435	GTGGAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGG	1494

Qy125X	601	AAAGATAGTGAAGGCAGTAATGATGACACTTTCATTTCCTTCCCACTACATCAGAACTGTAAACA	660
Db	1495	AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCGAAGCTGTGAAG	1554
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACCTGAGAATGTTTCA	720
Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCTTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTTCCCTTGTGTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTTCCCTTGTGTAGAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAG	1674
Qy	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
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Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAAACATGCCTGAAGGTCTAACCCAGATTTGGTTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCTATG	1139
Db	1972	TGCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCTTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCTGAGCATTCTGAGCTAGTT	1499

Qy	Db	Sequence	Qy	Db
1500	2329	GAAGATTCCCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559	2388
1560	2389	GAGGATTCCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCTTGAA	1619	2448
1620	2449	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1679	2507
1680	2508	TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAG	1739	2559
1740	2560	GGAGGAAAACCGTATTTTGGAGTCTTTTTCAGCCCAAGTTTAGGCATCACAAAAGATACCTTA	1799	2616
1800	2617	CTAGGAAAGCCATATTTAGAGTCTTTTTCAGCCCAATTTACATAGTACAAAAGATGC--T	1859	2676
1860	2677	GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAG	1919	2736
1920	2737	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1979	2796
1980	2797	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2039	2853
2040	2854	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	2099	2913
2100	2914	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTT	2159	2973
2160	2974	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	2219	3033
2220	2977	GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2279	3093
2280	2980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGACGGA	2339	3153
2340	2984	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTTCATTGCCTTGCTTAGAA	2399	3213
2400	2987	TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTTCATGTCCCAGAT	2459	3273
2460	2991	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2519	3333
2520	2994	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2579	3393
2580	2997	GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	2639	3453
2640	3001	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2699	3513
2700	3004	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	2759	3573
2760	3007	GCCGAGAGAAAACTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2819	3633
2820	3011	GCAGAGAAAAAACTTCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTG	2879	3693
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Db 3154 TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG 3213
 Qy 2340 ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT 2399
 |||||
 Db 3214 ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT 3273
 Qy 2400 GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA 2459
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 Qy 2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT 2519
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 Db 3514 GATTCCCTGAAGTTTGCA GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573
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 Db 3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTTGTTATTTATGAA 3633
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 |||||
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 Qy 2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG 2879
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 Qy 2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG 2939
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 Qy 2940 AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTA 2999
 ||
 Db 3798 GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTTA 3855
 Qy 3000 GCAACGCA0X| GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCTTTAAG 3059
 |||||
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 Qy 3060 TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG 3119
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 Db 3915 TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCAATGAGGC 3973
 Qy 3120 CACTGGTGAATAAAACAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT 3179
 |||||
 Db 3974 GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031

XX
 DE Human secreted protein BG160_1 cDNA.
 XX
 KW BG160_1; secreted protein; protein factor; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 102..2030
 FT /*tag= a
 FT sig_peptide 1863..1899
 FT /*tag= b
 FT /note= "putative leader/signal peptide"
 FT mat_peptide 1900..2027
 FT /*tag= c
 XX
 PN WO9817687-A2.
 XX
 PD 30-APR-1998.
 XX
 PF 24-OCT-1997; 97WO-US19590.
 XX
 PR 24-OCT-1997; 97US-0740274.
 PR 25-OCT-1996; 96US-0740274.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX
 DR WPI; 1998-261426/23.
 DR P-PSDB; AAW58383.
 XX
 PT Nucleic acid encoding secreted protein from human cells - useful,
 PT e.g. as immunomodulator, antitumour agent, promoters of tissue
 PT growth, haemostatic and thrombolytic agents etc.
 XX
 PS Claim 20; Page 74-75; 114pp; English.
 XX
 CC This cDNA clone, designated BG160_1, codes for a novel human
 CC secreted protein (see AAW58383). It was isolated from a human adult
 CC brain cDNA library using methods selective for cDNAs that encode
 CC secreted proteins. The clone is deposited in composite clone
 CC ATCC 98232; an oligonucleotide (see AAT99725) is designed to isolate
 CC the clone from the composite. The predicted AT415_4 amino acid
 CC sequence shows homology to neuroendocrine-specific proteins. Novel
 CC cDNA clones (see AAV30916-32) coding for human secreted proteins (see
 CC AAW58580-90) are claimed. These can be used for recombinant
 CC production of the secreted proteins for analysis, characterisation,
 CC diagnostic or therapeutic use. They can also be used as tissue or
 CC mol.wt. markers, for chromosome identification, to identify genetic
 CC disorders, to isolate new related DNA, as sources of primers for
 CC PCR, to generate antibodies, and in interaction trap assays. The
 CC secreted proteins may also have many biological activities, e.g.
 CC cytokine, immunomodulator, haematopoiesis regulating activity,
 CC tissue growth activity, activin or inhibin activity, chemotactic or
 CC chemokinetic activity, haemostatic and thrombolytic activity,

CC receptor/ligand activity, antiinflammatory, cadherin and tumour
CC invasion suppressor activity, and tumour inhibition activity. The
CC proteins can be expressed in vivo from DNA, introduced in gene
CC therapy vectors.

XX

SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;

Query Match 46.4%; Score 1777.2; DB 19; Length 2386;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 258; Indels 59; Gaps 11;

```
Qy      827 CAAGACATCAAACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
      ||| ||||| ||||| ||| | ||||| ||||| ||| ||||| ||| |||||
Db      2   CAAAACATCAAACCCCTTTCCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAAC 61

Qy      887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
      |||| | | | ||||| ||||| ||||| ||||| ||||| ||| | | |
Db      62  AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy      947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
      ||||| | | ||||| ||||| ||||| ||||| ||||| |||||
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Qy     1007 CTTTGAAACAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCC 1066
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      182 TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC 241

Qy     1067 TGTAACACAGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCGGTTTTGCC 1126
      || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      242 TGCAGCACAGCTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC 301

Qy     1127 TGACATTGTCATGGAAGCACCATTAAATTCGTAGTTCTTAGTGCTGGTGCTTCTGCAGT 1186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      302 TGACATTGTTATGGAAGCACCATTGAATTCGCAGTTCTTAGTGCTGGTGCTTCCGTGAT 361

Qy     1187 GCAGCTCAGTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT 1246
      |||| | | ||||| ||||| | ||||| ||||| ||||| |||||
Db      362 ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA 418

Qy     1247 TGAGCCTGAAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC 1306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      419 TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC 478

Qy     1307 AGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGA 1366
      ||||| | | ||||| | ||||| ||||| ||||| ||||| |||||
Db      479 AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA 538

Qy     1367 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC 1426
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      539 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC 598

Qy     1427 GACTCCAGATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCA 1486
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      599 AGCTCCGATTTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCCTGATCA 658

Qy     1487 TTCTGAGCTAGTTGAAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA 1546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Accession	Gene	Strain	Position	Sequence	Length
Db	659	TTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGA	718		
Qy	1547	TTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606		
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT	778		
Qy	1607	CAC TGAAATTT CATCTGAGTCAATGACAGGACATGACAATAAGGGAAAAC TCAGTGCTTC	1666		
Db	779	CAC TGAGACTT CATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAC TCAGTGCTTT	838		
Qy	1667	ACCATCACCTGAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCAC	1726		
Db	839	GC---CACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACAC	895		
Qy	1727	AAAAGATACCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTT	1786		
Db	896	AAAAGATACCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTT	955		
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGA	1846		
Db	956	GCAGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGA	1015		
Qy	1847	AGCAAACCTAAGAGAAAGTGAAACATTTTCAGATT CATCTCCGATTGAGATTATAGATGA	1906		
Db	1016	AGCACAGATAAGAGAAACTGAAACGTTTTCAGATT CATCTCCAATTGAAATATATAGATGA	1075		
Qy	1907	GTTCCCGACCTTTGTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC	1966		
Db	1076	GTTCCCTACATTGATCAGTTCTAAAACTGATT CATTTTCTAAATTAGCCAGGGAATATAC	1135		
Qy	1967	TGACCTAGAAGTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGT GTCATT	2026		
Db	1136	TGACCTAGAAGTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATT	1195		
Qy	2027	GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGT	2086		
Db	1196	GCCTTGACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA	1255		
Qy	2087	TCA-----TG TCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT	2140		
Db	1256	GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT	1315		
Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200		
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375		
Qy	2201	CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAAC TCTCTGATACAGAAAAAGAGCGAAG	2260		
Db	1376	CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAAC TCTCTCCGATACAGAAAAAGAGGACAG	1435		
Qy	2261	ATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTA	2320		
Db	1436	ATCACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTA	1495		
Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGT TGGTGCCAGCTTGTTCCCTGCTGCTCTC	2380		
Db	1496	CTGGAGAGACATTAAGAAGACTGGAGTGGTGT TGGTGCCAGCTTATCCTGCTGCTTTC	1555		

Qy	2381	GCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440
Db	1556	ATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441	GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
Db	1616	GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG	1675
Qy	2501	CCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	2560
Db	1676	CCACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	1720
Qy	2561	GTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTT	2620
Db	1721	GTACAGTAAATCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTT	1780
Qy	2621	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTA	2680
Db	1781	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTA	1840
Qy	2681	TGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAG	2740
Db	1841	TGTTGGTGCCTTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAG	1900
Qy	2741	TGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA	2800
Db	1901	TGTTCCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA	1960
Qy	2801	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA	2860
Db	1961	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA	2020
Qy	2861	AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT	2920
Db	2021	AGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT	2075
Qy	2921	TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTT	2980
Db	2076	TCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT	2134
Qy	2981	TCAC-----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCT	3028
Db	2135	TCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCT	2194
Qy	3029	GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAAA	3088
Db	2195	GTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAAA	2254
Qy	3089	TCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA	3148
Db	2255	CCGTAATCATA--TCTTTTTCTATCTGAGGCACTGGTGA-----ATAAAAAA	2301
Qy	3149	GCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG	3207
Db	2302	CCTGTATATTTTACTTTGTGTCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGG	2361

QY 3208 TGGAGCTGACAGAAATAA 3225
 ||||| | ||| ||
 Db 2362 TGGAGCTAGAAAAAAAAA 2379

RESULT 14

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US25135.

XX

PR 17-SEP-1999; 99US-0398829.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR, Spaulding V, tino M|||

XX

DR WPI; 2001-244801/25.

DR P-PSDB; AAB90682.

XX

PT Isolated nucleic acids encoding polypeptides, useful for modulating
 PT e.g. cytokine and cell proliferation/differentiation activity, the
 PT immune system and hematopoiesis regulating activity -

XX

PS Claim 1; Page 408-409; 557pp; English.

XX

CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; receptor/ligand activity; anti-inflammatory activity;
 CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
 CC tumour inhibition activity. Included in the invention are probes

CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.

XX

SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 other;

Query Match 46.3%; Score 1774; DB 22; Length 2386;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 260; Indels 59; Gaps 11;

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Qy      827 CAAGACATCAAACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
      ||| ||||||||||||||| ||| | ||||||||||| ||| ||||||||||| ||| |||||
Db       2 CAAAACATCAAACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC 61

Qy      887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
      |||| | | | ||||||||||| ||||||||||| ||||||||||| |||| | | |
Db       62 AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy      947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
      ||||| || | ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db      122 AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC 181

Qy     1007 CTTTGAAACAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCC 1066
      | ||||||||||||||| ||||||||||| ||||||| | ||| ||||||| |||
Db      182 TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC 241

Qy     1067 TGTAACACAGCTTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCC 1126
      || | ||||||||||||||| |||||||| | | ||||||||||| ||||| |||||||
Db      242 TGCAGCACAGCTTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC 301

Qy     1127 TGACATTGTTCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGT 1186
      ||||||||| ||||||||||||||| ||||||| ||||||||||||||||||||| | |
Db      302 TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT 361

Qy     1187 GCAGCTCAGTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT 1246
      |||| | | ||||||||||||||| | | ||||||||||||||||||||| |||
Db      362 ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA 418

Qy     1247 TGAGCCTGAAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC 1306
      ||||||||| ||||||||||||||| ||||||||||| ||||||||| ||||| |||
Db      419 TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC 478

Qy     1307 AGGAATGAATGAAGAAATCAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGA 1366
      |||||| | | |||||||| | ||||||||||| ||||| | | ||| ||||| |||
Db      479 AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGA 538

Qy     1367 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC 1426
      ||||||||||||||||||||||||||| ||||||||||| ||||| ||||| |||
Db      539 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC 598

Qy     1427 GACTCCAGATTTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCA 1486
      |||| | |||||||| | ||||||||||| ||| ||||||| ||||||||||| |||
Db      599 AGCTCCGATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCA 658

Qy     1487 TTCTGAGCTAGTTGAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA 1546
      ||||||||||||||||||||| || ||||||||| ||||||||| ||||| |||
Db      659 TTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA 718
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Qy	1547	TTCAATATCCCGAAGTTCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCT	778
Qy	1607	CACTGAAATTTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTC	1666
Db	779	CACTGAGACTTCATTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACCTCAGTGCTTT	838
Qy	1667	ACCATCACCTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCAC	1726
Db	839	GC---CACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACAC	895
Qy	1727	AAAAGATACCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTT	1786
Db	896	A TACCCAGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTT	955
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGA	1846
Db	956	GCAGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGA	1015
Qy	1847	AGCAAACCTAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGA	1906
Db	1016	AGCACAGATAAGAGAAAAGTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGA	1075
Qy	1907	GTTCCCGACCTTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC	1966
Db	1076	GTTCCCTACATTGATCAGTTCTAAAAGTATTTCATTTTCTAAATTAGCCAGGGAATATAC	1135
Qy	1967	TGACCTAGAAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATT	2026
Db	1136	TGACCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATT	1195
Qy	2027	GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGT	2086
Db	1196	GCCTTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA	1255
Qy	2087	TCA-----TGTCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT	2140
Db	1256	GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT	1315
Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375
Qy	2201	CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAG	2260
Db	1376	CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAG	1435
Qy	2261	ATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTA	2320
Db	1436	ATCACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTA	1495
Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTC	2380
Db	1496	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTC	1555
Qy	2381	GCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440

Db	1556		ATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441		GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
Db	1616		GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG	1675
Qy	2501		CCACCCATTTCAGGGCATAATTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	2560
Db	1676		CCACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	1720
Qy	2561		GTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTT	2620
Db	1721		GTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTT	1780
Qy	2621		CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA	2680
Db	1781		CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA	1840
Qy	2681		TGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAG	2740
Db	1841		TGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAG	1900
Qy	2741		TGTTCTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA	2800
Db	1901		TGTTGGTGTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA	1960
Qy	2801		TAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA	2860
Db	1961		TAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA	2020
Qy	2861		AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT	2920
Db	2021		AGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT	2075
Qy	2921		TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAAACAAAGCCTTGACATTGCAGTGCAGTT	2980
Db	2076		TCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT	2134
Qy	2981		TCAC-----AGATCTTTATTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCT	3028
Db	2135		TCACAGATCGTTGTTAGATCTTTATTTTAGCCATGCACTGTTGTGAGGAAAAATTACCT	2194
Qy	3029		GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	3088
Db	2195		GTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	2254
Qy	3089		TCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA	3148
Db	2255		CCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGCTGGA-----ATAAAAAA	2301
Qy	3149		GCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG	3207
Db	2302		CCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGG	2361
Qy	3208		TGGAGCTGACAGAAATAA 3225	

Qy	1446	TATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGAT	1505
Db	148	TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTAGTTGAAGAT	207
Qy	1506	TCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCA	1565
Db	208	TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA	267
Qy	1566	CAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCATCTGAG	1625
Db	268	CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAG	327
Qy	1626	TCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGGGAGGA	1685
Db	328	TCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTTGC---CACCTGAGGGAGGA	384
Qy	1686	AAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAGCACCT	1745
Db	385	AAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTGTACCT	444
Qy	1746	GATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGCTCAAT	1805
Db	445	GATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTCAGT	504
Qy	1806	ACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAGAAAGT	1865
Db	505	ACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAACT	564
Qy	1866	GAAACATTTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTGTCTCAGT	1925
Db	565	GAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGT	624
Qy	1926	TCTAAAGCAGATTCTTCTCTACATTAGCCAGGGAATACACTGACCTAGAAGTAGCCAC	1985
Db	625	CCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCAC	684
Qy	1986	AAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGATTGCCC	2045
Db	685	AAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTGCCC	744
Qy	2046	CATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCATGTCCAGAT	2099
Db	745	CATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGAT	804
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159
Db	805	GACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCT	864
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	865	GCTTTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAA	924
Qy	2220	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	925	GCTGAGAAAAAATTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTT	984

Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	985	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAG	1044
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	1045	ACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCAGCTGCTTTTCATTGACAGTATTCAGCATT	1104
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	1105	GTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATA	1164
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATAT	2519
Db	1165	TA00XA TGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATAT	2022
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	1225	CTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTT	1284
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	1285	GGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTT	1344
Qy	2640	GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	1345	GATTCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAT	1404
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAA	2759
Db	1405	GGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTGTTATTTATGAA	1464
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	1465	CGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCT	1524
Qy	2820	ATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	1525	ATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCA	1584
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG	2939
Db	1585	AAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGG	1639
Qy	2940	AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----AGAT	2988
Db	1640	AGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGAT	1698
Qy	2989	CTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTT	3047
Db	1699	CTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTT	1758
Qy	3048	CATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTT-	3106
Db	1759	CATCATCTTAAGTATTGTAAGCTGCTATGTATGGGTTTAAACCGTAATCATATCTTTTTC	1818
Qy	3107	-TTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTT	3165

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Db    1819 CTATCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATTTTACTTT 1867

Qy    3166 GTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATA 3224
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Db    1868 GTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAA 1927

Qy    3225 A 3225
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Db    1928 A 1928

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Search completed: January 23, 2004, 03:14:29
Job time : 929.523 secs

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:43:47 ; Search time 194.332 Seconds
 (without alignments)
 8705.823 Million cell updates/sec

Title: US-09-830-972-28
 Perfect score: 3833
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 sum CCGATG

Database : Issued_Patents_NA:*
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 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2687.8	70.1	799	4	US-09-484-970B-106	Sequ 6, App
2	590.8	15.4	799	2	US-08-700-607-2	Sequence 2, Appli
3	230.4	6.0	1766	4	US-09-149-476-254	Sequence 254, App
4	230.4	6.0	2664	4	US-09-149-476-255	Sequence 255, App
5	202.2	5.3	1095	2	US-08-700-607-4	Sequence 4, Appli
6	182	4.7	794	4	US-09-149-476-102	Sequence 102, App
7	174.2	4.5	261	2	US-08-700-607-9	Sequence 9, Appli
8	138.6	3.6	301	4	US-09-439-313-279	Sequence 279, App
9	138.6	3.6	301	4	US-09-352-616A-279	Sequence 279, App
10	138.6	3.6	301	4	US-09-232-149A-279	Sequence 279, App
11	113.6	3.0	211	4	US-09-506-729-51	Sequence 51, Appl

c	12	69.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	13	60.8	1.6	200	3	US-09-221-298-100	Sequence 100, App
	14	46.6	1.2	3095	6	5231168-1	Patent No. 5231168
	15	44	1.1	1134	3	US-09-248-335-29	Sequence 29, Appl
c	16	43.8	1.1	1949	4	US-08-961-527-289	Sequence 289, App
	17	43.6	1.1	2439	3	US-09-386-493-1	Sequence 1, Appli
c	18	42.8	1.1	949	3	US-08-714-918-12	Sequence 12, Appl
c	19	42.8	1.1	949	3	US-09-265-315-12	Sequence 12, Appl
c	20	42.8	1.1	949	3	US-09-265-315-12	Sequence 12, Appl
c	21	42.8	1.1	949	3	US-09-266-417-12	Sequence 12, Appl
c	22	42.8		1739	3	US-08-714-918-1	SequenceG1, Appl129875XG
c	23	42.8	1.1	1739	3	US-09-265-315-1	Sequence 1, Appli
c	24	42.8	1.1	1739	3	US-09-265-315-1	Sequence 1, Appli
c	25	42.8	1.1	1739	3	US-09-266-417-1	Sequence 1, Appli
	26	42.4	1.1	2671	6	5168051-9	Patent No. 5168051
	27	42	1.1	277	3	US-09-007-005-3	Sequence 3, Appli
	28	42	1.1	277	3	US-09-244-796-3	Sequence 3, Appli
	29	41.6	1.1	21234	4	US-09-810-671-3	Sequence 3, Appli
	30	41.4	1.1	978	4	US-09-107-532A-2099	Sequence 2099, Ap
	31	41.2	1.1	2529	2	US-08-867-129-1	Sequence 1, Appli
	32	40.8	1.1	3763	1	US-07-792-865D-1	Seq Appli
	33	40.6	1.1	425	3	US-08-905-223-178	Sequence 178, App
	34	40.6	1.1	1989	4	US-09-134-001C-1237	Sequence 1237, Ap
	35	40.4	1.1	5181	1	US-08-257-073-10	Sequence 10, Appl
	36	40.2	1.0	248	3	US-09-007-005-32	Sequence 32, Appl
	37	40.2	1.0	248	3	US-09-244-796-32	Sequence 32, Appl
	38	39.8	1.0	20674	4	US-09-641-638-651	Sequence 651, App
	39	39.6	1.0	1342	4	US-09-489-847-89	Sequence 89, Appl
	40	39.6	1.0	2610	4	US-09-545-814-1	Sequence 1, Appli
c	41	39.6	1.0	2610	4	US-09-545-814-3	Sequence 3, Appli
	42	39.6	1.0	3211	2	US-08-574-959A-8	Sequence 8, Appli
	43	39.6	1.0	32		-09-357-014-8	Sequence 8, Appli
	44	39.6	1.0	3602	4	US-09-402-929-1	Sequence 1, Appli
	45	39.6	1.0	3901	2	US-08-574-959A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

; Patent No. 6426186

; GENERAL INFORMATION:

; APPLICANT: Jones, Karen A.

; APPLICANT: Volkmuth, Wayne

; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES

; FILE REFERENCE: PB-0014 US

; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PERL Program

; SEQ ID NO 106

; LENGTH: 4822

; TYPE: DNA

; ORGANISM: Homo sapiens

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Db	1618	GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1677
Qy	718	TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1678	GCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	1737
Qy	778	AAGA--TAGAAAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db	1738	AAAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC	1797
Qy	836	AAACCC-TTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATG	894
Db	1798	AAACCCTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATT	1857
Qy	895	TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGG	954
Db	1858	TAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAG	1917
Qy	955	TTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAA	1014
Db	1918	TACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAA	1977
Qy	1015	CAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACAC	1074
Db	1978	CAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCAC	2037
Qy	1075	AGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACCGTTTTGCCTGACATTG	1134
Db	2038	AGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTG	2097
Qy	1135	TCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCA	1194
Db	2098	TTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCA	2157
Qy	1195	G TTCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTG	1254
Db	2158	GCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTG	2214
Qy	1255	AAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGA	1314
Db	2215	AAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAA	2274
Qy	1315	ATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTT	1374
Db	2275	AGGAAGAAATTAAAGAGCCTGAAAATATTAAATGCAGCTCTTCAAGAAACAGAAGCTCCTT	2334
Qy	1375	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAG	1434
Db	2335	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGG	2394
Qy	1435	ATTTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGC	1494
Db	2395	ATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGC	2454
Qy	1495	TAGTTGAAGATTTCCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGTATGATTCAATAC	1554

Db	2455	 TAGTTGAAGATTCTTCACTGATTCTGAACCACTTCACTTATTTAGTGATGATTCAATAC	2514
Qy	1555	CCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAA	1614
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Qy	1615	TTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCAC	1674
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Qy	1675	CTGAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATA	1734
Db	2632	CTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATA	2691
Qy	1735	CCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGG	1794
Db	2692	CCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGG	2751
Qy	1795	AGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCACTGCTCAGGAAGCAAACC	1854
Db	2752	AGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGA	2811
Qy	1855	TAAGAGAAAGTGAAACATTTTCAGATTCACTCCGATTGAGATTATAGATGAGTTCCCGA	1914
Db	2812	TAAGAGAAACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCCTA	2871
Qy	1915	CCTTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAACTGATTCACTTTCTAAATTAGCCAGGGAATATACTGACCTAG	2931
Qy	1975	AAGTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCACTGGCTTGTG	2034
Db	2932	AAGTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCACTGCCTTGCA	2991
Qy	2035	CAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088
Db	2992	CAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCA	3051
Qy	2089	ATGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTC	2148
Db	3052	GTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTC	3111
Qy	2149	CAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTC	2208
Db	3112	CAGATGTSEQT6KHTTGG TCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTC	3171
Qy	2209	TTGTGAAAGAAGCCGAGAGAAAACTTCCTTCGATACAGAAAAAGAGCGAAGATCTCCAT	2268
Db	3172	TTGTGAAAGAAGCTGAGAAAAAACTTCCTTCGATACAGAAAAAGAGGACAGATCACCAT	3231
Qy	2269	CTGCTATATTTTCAGCAGAGCTGAG-TAAAACTTCAGTTGTTGACCTCCTCTACTGGAGA	2327
Db	3232	CTGCTATATTTTCAGCAGAGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGA	3291
Qy	2328	GACATTAAGAAGACTGGAGTGGTGTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACA	2387

Db 3292 GACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACA 3351
 Qy 2388 GTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATC 2447
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 Db 3352 GTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATC 3411
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 Db 3412 AGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCA 3471
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 Db 3532 AATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTT 3591
 Qy 2628 GATGATTTAGTTGATTCTCTGAAGT'TTGCAGTGT'TGATGTGGGTATTTACCTATGTTGGT 2687
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 Db 3592 GATGATTTAGTTGATTCTCTGAAGTTTGCAGTGT'TGATGTGGGTATTTACCTATGTTGGT 3651
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 Db 3652 GCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCT 3711
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 Db 3712 GTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAAT 3771
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 Db 3772 GTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 3831
 Qy 2868 TGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTTG 2927
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 Db 3832 TGAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCAATTTG 3886
 Qy 2928 ATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC--- 2984
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 Db 3887 ATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGA 3945
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 Db 3946 TCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA 4005
 Qy 3036 CTXT TTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAAT 3092
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 Qy 3096 CATATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTAT 3155
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 Db 4066 CATA--TCTTTTCTCTATCTGAGGCACTGGTGGG-----ATAAAAAACCTGTAT 4112
 Qy 3156 ATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
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```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

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Query Match          15.4%; Score 590.8; DB 2; Length 799;
Best Local Similarity 92.9%; Pred. No. 9e-139;
Matches 643; Conservative 0; Mismatches 42; Indels 7; Gaps 2;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
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Db      168 CTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 227
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Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Db      228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287
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Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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Db      288 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347
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Qy      2544 GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
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Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
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Db	468	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	527
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	528	CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	587
Qy	2784	TATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
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Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
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RESULT 3

US-09-149-476-254

; Sequence 254, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZX6 P1

9

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

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; EARLIER APPLICATION NUMBER: 60/047,600

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; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 1766;
Best Local Similarity 63.6%; Pred. No. 3.8e-48;
Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Qy      2420 TGCCTTGGCCCTGCTCTCTGTGACTATC1 TAGGATATATAAGGGTGTGATCCAGGC 2476
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RESULT 4

US-09-149-476-255

; Sequence 255, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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 ; EARLIER APPLICATION NUMBER: 60/061,060
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 Qy 2360 CAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACAT 2419
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 Db 321 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTTCTTACCT 380
 Qy 2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
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 Db 381 CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 440
 Qy 2480 TATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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 Db 441 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 500
 Qy 2540 ATCTGAGGAGTTGGTTTCAAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAAT 2599
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 Db 501 GTCCTCAGAAGCTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 560
 Qy 2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
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 Db 561 GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 620
 Qy 2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTT 2719
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 Db 621 CTTCATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCTTCTAATTCT 680

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Qy 2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
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Qy 2540 ATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAT 2599
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RESULT 6
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/056,884
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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          4.7%; Score 182; DB 4; Length 794;
Best Local Similarity 61.2%; Pred. No. 3.7e-36;
Matches 333; Conservative 6; Mismatches 201; Indels 4; Gaps 3;
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Qy      2300 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 2359
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Db      253 TGCGGTGACCTGCTGATTCTGAGAXo GAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy      2360 CAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCC-TACA 2418
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Db      311 CACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGCATCARTGTGGGTTTCTTAMC 370

Qy      2419 TTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGG 2478
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Db      371 TCATCCTGGCTCTTCTCTGTGACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy      2479 CTATCCAGAAATCTGATGAAGGCCACCCATT-CAGGGCATATTTGGAATCTGAAGTTGCT 2537
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Qy      2538 ATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACA 2597
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Qy      2598 ATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCA 2657
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Qy      2658 GTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATT 2717
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US-08-700-607-9

US-08-700-607-9

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Db          287 ATTTCA TTGCACAGA 301

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RESULT 9

US-09-352-616A-279

; Sequence 279, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

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; APPLICANT: Harlocker, Susan Louise
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; APPLICANT: Jiang, 750Xi

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C8

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; CURRENT APPLICATION NUMBER: US/09/352,616A|||||ataxia806Xe

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840
84

; NUMBER OF SEQ ID NOS: 472

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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEO ID NO 279

; LENGTH: 301

TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

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; NAME/KEY: misc feature
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; LOCATION: (1)...(301)

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OTHER INFORMATION: n = A,T,C or G

US-09-352-616A-279

Query Match 3.6%; Score 138.6; DB 4; Length 301;

Best Local Similarity 80.3%; Pred. No. 1.9e-25;

Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;

Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTAC 3373
|||

Db 1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy 3374 TGTGTGTTAATTGCGCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTC 3433

Db 60 TGT TAT ATTA ATTGCCAATATAAGTAAATATAGATTATA-----TATGTATAGTGTTTC 113

QY 3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGT 3487

Db 114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTCAGAGTCAGT 172

Qy	3488	CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAAACGTACTTCTA-GG	3546
Db	173	CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAATATTCTAGGG	232
Qy	3547	CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA	3606
Db	233	AGCACTACCATCTGTTTTCA- - -CATGAAATGCCACACACATAGAAGTC- -CAACATCA	286
Qy	3607	ACTTCACTGCACAGA	3621
Db	287	ATTTTCATTGCACAGA	301

RESULT 10

US-09-232-149A-279

; Sequence 279, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER: US/09/232,149A

; CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

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; SOFTWARE: FastSEO for Windows Version 3.0
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; SEQ ID NO 279

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; LENGTH: 301

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; TYPE: DNA

; ORGANISM: Homo sapien

FEATURE:

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; NAME/KEY: misc feature
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; LOCATION: (1)...(301)

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;      LOCATION: (1,1) (SEE)
;      OTHER INFORMATION: n = A,T,C or G

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US-09-232-149A-279

Query Match 3.6%; Score 138.6; DB 4; Length 301;

Best Local Similarity 80.3%; Pred. No. 1.9e-25;

Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;

QY 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTAC 3373
||| ||| |
Db 1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

A Qy 3374 TGTGTTATTAATTGCCA AGTAAATAAGATTATATATCTATATATAGTGTTTT 3433
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 TGTATATTAATTGCCAATATAAGTAAATATAGATTATA-----TATGTATAGTGTTTT 113

QY 3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGT 3487
|| ||||||| |||||||| | ||| ||||||||| ||||| |
Db 114 ACAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy 3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546

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Db      173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAATATTTCTAGGG 232

Qy      3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
          |||||||||||||||| | ||| | | |||||| | ||||| |
Db      233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy      3607 ACTTCACTGCACAGA 3621
          | ||| | |||||
Db      287 ATTTCACTGCACAGA 301

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RESULT 11

US-09-506-729-51

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; Sequence 51, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; TITLE OF INVENTION: GRANULOCYTIC CELLS
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-51

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Query Match          3.0%; Score 113.6; DB 4; Length 211;
Best Local Similarity 78.0%; Pred. No. 3e-19;
Matches 167; Conservative 0; Mismatches 34; Indels 13; Gaps 2;

```

```

Qy      2986 GATCTTTATTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTG 3045
          |||||||||||||||| | ||| | | |||| | |||||| | ||||| |
Db      1 GATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGTG 60

Qy      3046 TTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTT 3105
          *p77$Xt$ |||||||||||||||||||||||||||||||||| |||
Db      61 TTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATATCTTTT 120

Qy      3106 T--TTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACT 3163
          | | || | |||||||||||| | | | ||||||| |||
Db      121 TCCTATCTATCTGAGGCACTGGTGA-----ATAAAGAACCTGTATATTTTACT 169

Qy      3164 TTGTCGCAGGTAGTCTTGCTGTATTTGGGGAATT 3197
          |||| |||| |||||||| | || | || ||
Db      170 TTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGT 203

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Db      1464 AGTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1405
Qy      294 TAGTCTTAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGA 353
      :: :: : : : : : : : : : : : : : : : : : :
Db      1404 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1345
Qy      354 AGAAGAAGATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGT 413
      :::::::::: : : : : : : : : : : : : : : : : : :
Db      1344 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1285
Qy      414 TGCAGCAGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATG 473
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      1284 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1225
Qy      474 GGAAGTGAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGA 533
      7 TTCTCTAGTT:: : : : : : : : : : : : : : : : : :
Db      1224 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1165
Qy      534 GAGCAAATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAA 593
      :: : : : : : : : : : : : : : : : : : : : : : :
Db      1164 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1105
Qy      594 TCGTGAAAAAGATAGTGAAAGCAGTAATGATGA 626
      : : : : : : : : : : : : : : : : : : : :
Db      1104 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1072

```

RESULT 13

US-09-221-298-100

; Sequence 100, Application US/09221298

; Patent No. 6284241

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER

; FILE REFERENCE: 210121.471

; CURRENT APPLICATION NUMBER: US/09/221,298

; CURRENT FILING DATE: 1998-12-23

; N| SEQ ID NOS: 112

|||| ||0

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 100

; LENGTH: 200

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (3)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (5)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (6)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

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; NAME/KEY: modified_base
; LOCATION: (14)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (21)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (23)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (29)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Where n is a, c, g or t
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; NAME/KEY: modified_base
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; OTHER INFORMATION: Where n is a, c, g or t
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; NAME/KEY: modified_base
; LOCATION: (166)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (176)
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; NAME/KEY: modified_base
; LOCATION: (185)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (186)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (195)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-221-298-100

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Query Match          1.6%;  Score 60.8;  DB 3;  Length 200;
Best Local Similarity 66.5%;  Pred. No. 5.2e-06;
Matches 111;  Conservative 0;  Mismatches 48;  Indels 8;  Gaps 2;

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Qy      3517 ACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCG 3576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 ACNTNNACTAGAANTAACAGNCNTTCTANGAACACTACCATCTGTNTTCACATGAAATGC 60

Qy      3577 ACGCCATGCAAAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAAT 3636
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61 CACACACATANAAA-----CTCCAACATCAATTTTCATTGCACAGACTGACTGTAATTAAT 115

Qy      3637 TTTATCAC---AAACTCTGGACTGAATCTAATGCTTCCAAAATGTT 3680
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      116 TTTGTCACAGGAATCTATGGACTGAATCTAATGCNNCCCCAAATGTT 162

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RESULT 14

5231168-1

;Patent No. 5231168

; APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;

;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.

; TITLE OF INVENTION: MALARIA ANTIG

GA

; NUMBER OF SEQUENCES: 19

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/409,658

; FILING DATE: 18-SEP-1989

;SEQ ID NO:1:

; LENGTH: 3095

5231168-1

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Query Match      1.2%; Score 46.6; DB 6; Length 3095; 1464
Best Local Similarity 47.2%; Pred. No. 0.067;
Matches 142; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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Qy      1285 ATGTATCACTAAAAAAGAATCAGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTA 1344
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      359 AAGAATCAGGTGAAAGTGGATTAGTTGATAATGAAGAAGGTGATTTTGAAGAACCTAATC 418

Qy      1345 GTGTAGCTGTTTCAGGAAAACAGAAGCTCCTTATATATCTATTGCATGTGATTTAATTAAAG 1404
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      419 ATGAAGAATTTGAACCTGATCAAAATGACTCTGAATTAAGTGAATTAAGTTAGTTGAAT 478

Qy      1405 AAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGTT
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      479 CAGAAAAAAGTGTATCTGAACCGACTGAACATGTAGAAATTGTATCAGAAAAAAGTGTAT 538

Qy      1465 TTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGATTCCTCCCCGATTCTGAAC 1524
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      539 CTGAACCGCTGAACACGTAGAAATTGTATCTGAAAAAAGTACATCCGAACCGCTGAAC 598

Qy      1525 CAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTG 1584
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      599 ATGTAGAAAGTGTATCTGAACAAAGTAATAACGAACCATCCGAAAAGAAAGATGGACCAG 658

Qy      1585 T 1585
      |
Db      659 T 659

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RESULT 15

US-09-248-335-29

; Sequence 29, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 29
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-29

Query Match 1.1%; Score 44; DB 3; Length 1134;
Best Local Similarity 61.2%; Pred. No. 0.19;
Matches 71; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy      3718 TGACGATTATACAAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTG 3777
          ||  |||| |  ||||| | || | |||| | | | || || || | ||
Db      971 TGGGTATTTGTTGTATTGTGATGTACGGAGTATTCATCAACTCCTTTTGCAAGATTGGTC 1030

Qy      3778 AACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
          || | | | |||| | || || | | | ||||| ||||| |||||
Db     1031 AATTATTCAGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1086
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Search completed: January 23, 2004, 15:31:22
Job time : 196.332 secs

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:28:33 ; Search time 1153.34 Seconds
(without alignments)
11885.997 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY ~~NECXA~~ /2/pubpna/US10A_PUBCOMB.seq:* AC TCA 1545
Gapop 10.0 , Gapext 1.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 4713738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

5 Listing first 45 mmaries AG

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cg
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

	1	2649.8	69.1	4632	15	US-10-060-036-53	Sequence 53, Appl
	2	2379.4	62.1	4053	9	US-09-758-140-5	Sequence 5, Appli
	3	2379.4	62.1	4053	9	US-09-972-599A-5	Sequence 5, Appli
	4	2223.6	58.0	3579	9	US-09-789-386-1	Sequence 1, Appli
	5	2223.6	58.0	3579	9	US-09-893-348-22	Sequence 22, Appl
	6	2179.4	56.9	4684	9	US-09-893-348-17	Sequence 17, Appl
	7	1414.6	36.9	1980	13	US-10-220-891-22	Sequence 22, Appl
	8	1025.4	26.8	2235	15	US-10-060-036-54	Sequence 54, Appl
	9	915.6	23.9	1785	12	US-10-439-388-62	Sequence 62, Appl
	10	826.4	21.6	2782	13	US-10-205-194-165	Sequence 165, App
	11	685.8	17.9	1610	9	US-09-765-205-5	Sequence 5, Appli
	12	683	17.8	1160	15	US-10-175-523-156	Sequence 156, App
	13	538.8	14.1	868	9	US-09-789-386-3	Sequence 3, Appli
c	14	535	14.0	4710	11	US-09-764-891-7385	Sequence 7385, Ap
	15	527	13.7	1122	9	US-09-789-386-5	Sequence 5, Appli
	16	484.6	12.6	972	13	US-10-437-931-1	Sequence 1, Appli
	17	464	12.1	472	10	US-09-983-965-507	Sequence 507, App
	18	443.4	11.6	459	14	US-10-079-623-238	Sequence 238, App
	19	427.2	11.1	447	10	US-09-983-965-190	Sequence 190, App
	20	427	11.1	441	10	US-09-983-965-3801	Sequence 3801, Ap
	21	423.8	11.1	429	10	US-09-983-965-2991	Sequence 2991, Ap
	22	422	11.0	422	10	US-09-960-352-8477	Sequence 8477, Ap
	23	418.8	10.9	422	10	US-09-960-352-11567	Sequence 11567, A
	24	398	10.4	406	10	US-09-983-965-293	Sequence 293, App
	25	383.4	10.0	423	10	US-09-960-352-9092	Sequence 9092, Ap
	26	354.4	9.2	389	10	US-09-960-352-5154	Sequence 5154, Ap
	27	352.2	9.2	357	10	US-09-983-965-2974	Sequence 2974, Ap
	28	337.4	8.8	3413	14	US-10-001-843-61	Sequence 61, Appl
c	29	316.6	8.3	3413	14	US-10-001-843-61	Sequence 61, Appl
	30	300.4	7.8	302	10	US-09-983-965-72	Sequence 72, Appl
	31	277.6	7.2	668	12	US-10-264-237-163	Sequence 163, App
	32	270	7.0	431	10	US-09-960-352-2205	Sequence 2205, Ap
	33	267.6	7.0	1520	15	US-10-084-817-333	Sequence 333, App
	34	266.8	7.0	3202	10	US-09-954-456-210	Sequence 210, App
	35	255.8	6.7	262	14	US-10-079-623-283	Sequence 283, App
	36	254.4	6.6	1502	13	US-10-205-219-94	Sequence 94, Appl
	37	251	6.5	263	10	US-09-983-965-5543	Sequence 5543, Ap
	38	250.4	6.5	1473	13	US-10-205-194-128	Sequence 128, App
	39	233.8	6.1	330	14	US-10-040-739-366	Sequence 366, App
	40	231.8	6.0	3637	12	US-10-108-260A-449	Sequence 449, App
	41	231.8	6.0	363		-10-159-563-443	Sequence 443, App
	42	230.4	6.0	1330	15	US-10-106-698-1945	Sequence 1945, Ap
	43	230.4	6.0	1656	9	US-09-729-674-19	Sequence 19, Appl
	44	230.4	6.0	1668	9	US-09-765-205-25	Sequence 25, Appl
	45	230.4	6.0	1766	11	US-09-809-391-254	Sequence 254, App

ALIGNMENTS

RESULT 1

US-10-060-036-53

; Sequence 53, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

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Query Match 69.1%; Score 2649.8; DB 15; Length 4632;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	853	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	912
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTTCTCA	120
Db	913	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	972
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAAATTGGAATAT	180
Db	973	GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC	1032
Qy	181	TCAGAAATGGAATCATCATTCACTGAGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1033	TCAGAAATGGGATCATCGTTCACTGAGGCTCTCAAAGGCAGAACCTGCCGTAATAGTAGCA	1092
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1093	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTAAGGAAAAGGGAGTTTCAGCA	420
Db	1213	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1269
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1270	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1329
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTA	540
Db	1330	AAAGATAGT---AAGGAAGATAGTGATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAAC	1386

5XC

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1387	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1446
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1447	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1506
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1507	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1566
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGAAAAATAAGACAGATGAAAAA	777
Db	1567	GSOURCE: 425XDTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1626
Qy	778	AAGATAGAA-AAAAAAGGCCAAATTGTAAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1627	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1686
Qy	837	AACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1687	AACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1746
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1747	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1806
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA	1016
Db	1807	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1866
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1867	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1926
Qy	1077	CTTTGCCCATCTTTTGAAGAACTCTGAAGCTACTCCGTACCGGTTTTGCCTGACATTGTC	1136
Db	1927	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1986
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1987	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2046
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
		AAT	
Db	2047	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2103
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2104	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2163
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376
Db	2164	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2223

Qy	1377	ATATCTATTGTCATGTGATTTTAATTAAAGAAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2224	ATATCTATTGTCATGTGATTTTAATTAAAGAAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2283
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTTCTGAGCTA	1496
Db	2284	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTTCTGAGCTA	2343
Qy	1497	GTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGTATGATTCAATACCC	1556
Db	2344	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGTATGATTCAATACCT	2403
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404	CAAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2463
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTTACCATCACCT	1676
Db	2464	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCCTTGC---CACCT	2520
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2580
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2640
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2641	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2700
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2760
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2820
Qy	1977	GTAGCCCAACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2821	GTATCCCAACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCATTGCCTTGCA	2880
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2940
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2941	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTCCTCCA	3000
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3060
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	3061	 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3120
Qy	2271	 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3121	 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3180
Qy	2331	 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3181	 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3240
Qy	2391	 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3241	 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3300
Qy	245		
Db	3301	 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3360
Qy	2511	 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3361	 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3420
Qy	2571	 TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3421	 TCTGCTCTTGGTCATGTGAAC TGACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3480
Qy	2631	 GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3481	 GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTAT	540
Qy	2691	 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3541	 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3600
Qy	2751	 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3601	 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3660
Qy	2811	 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3661	 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3720
Qy	2871	 GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTTGATT	2930
Db	3721	 AAACGCCCAAAATAATTAGT-----AGGAGTTTCATCTTTAAAGGGGATATTCAATTTGATT	3775
Qy	2931	 CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCT	2990
Db	3776	AT-----ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCATCTATAC	38105XT 3785
Qy	2991	 TTATTTT TAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGA CTGCCCTGTGTTCA	3049
Db	3786	 TTATTTT TAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA CTGCCATGTGTTCA	3845
Qy	3050	 TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTC	3109


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; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (KIAA0886,
GenBank
; OTHER IN
US-09-758-140-5

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Query Match G DATE: cc62s10p 88co0820020012965A19AB020698h 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
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Db      846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      906 GTATTACCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy      121 GAGAAGGCAAAAATCCATTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      966 GAGAA      AAATCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1005

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1026 TCAGAAATGGGATCATCGTTCAGTGTCTCTCAAAGGCAGAACTGCCGTAATAGTAGCA 1085

Qy      241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

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Qy	361	GATAGAGTTCTGTCTCCAGCAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1206	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1262
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1263	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1322
Qy	481	AAAGATACTTACAAGCAAGATAGTGTGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGTATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	AAGTGGATAAAAAATGTTTTTCAGATAGAGTGTGAGTGGAGTAAATCGAGAGCAAC	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTCCCCAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	717
Db	1500	GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTCCCTTGTTAGGAGATCTTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1679
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCCTTTTCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256

Db 2040 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAAATGAGCCTGAA 2096
 Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
 Db 2097 AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG 2156
 Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGAAGCTCCTTAT 1376
 Db 2157 GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT 2216
 Qy 1377 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 1436
 Db 2217 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT 2276
 Qy 143
 Db 2277 TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA 2336
 ATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTAGAGATA 599650XC
 Qy 1497 GTTGAAGATTTCCTCCCCGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCC 1556
 Db 2337 GTTGAAGATTTCCTCACCTGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCT 2396
 Qy 1557 GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT 1616
 Db 2397 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT 2456
 Qy 1617 TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT 1676
 Db 2457 TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTG8---CACCT 2513
 Qy 1677 GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC 1736
 Db 2514 GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC 2573
 Qy 1737 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG 1796
 Db 2574 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAG 2633
 Qy 1797 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA 1856
 Db 2634 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA 2693
 Qy 1857 AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC 1916
 Db 2694 AGAGAAAAGTGAAACGTTTTTC ATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA 2753
 Qy 1917 TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA 1976
 Db 2754 TTGATCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATATACTGACCTAGAA 2813
 Qy 1977 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCA 2036
 Db 2814 GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGCACA 2873
 Qy 2037 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT 2090

Db	2874	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAAATCAGT	2933
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTCTGCTGCTCTCGCTGACAGTA	2390
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353
Qy	2511	AGGATCATCTCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCA5XA	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAACTGCACGATAAAAGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3534	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3593
Qy	2751	ATTTATGAACGGCATCA1	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3654	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3714	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3768


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Qy      2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC----- 2984
      |  |||||||||||||||||||  ||  |||||||  |||||||||||||||||||
Db      3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827

Qy      2985 -----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGA CTG 3038
      |||||||||||||||||||  ||  ||  ||  |||||||||||||||||||
Db      3828 TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA CTG 3887

Qy      3039 CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
      ||  |||||||||||||||||||  |||||||||||||||||||  |||||||
Db      3888 CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3947

Qy      3099 ATTTGTTTTTTCCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT 3158
      |  |  |||||||  |  |||||||||||||||  |  |  ||  |||||||
Db  1      8 A--TCTTTTTCTATCTGAGGCACTGGTGA-----AAATGAAAAAAGCTGTATATT 3994

Qy      3159 ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
      |||||||  |||  |||||||  ||  ||  |||  |  |||||  ||  |||||||
Db      3995 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4051

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RESULT 3

US-09-972-599A-5

; Sequence 5, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/758,140

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/236,378

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/207,366

CCT5 418

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/175,707

; PRIOR FILING DATE: 2000-01-12

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 4053

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (135)..(3710)

; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein (KIAA0886, GenBank

; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)

US-09-972-599A-5

Query Match

62.1%; Score 2379.4; DB 9; Length 4053;

Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy     61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy    121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    966 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1025

Qy    181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAA4          TGCCGTAACAGTAAAG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1026 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085

Qy    241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy    301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy    361 GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTAAAGGAAAAGGGAGTTGCAGCA 420
      ||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1206 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAAATGAAAAGAGAGTTGCAGTG 1262

Qy    421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1263 GAAGCTCCTATGAGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG 1322

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1323 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1379

Qy    541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1380 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1439

Qy    601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1440 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1499

Qy    661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
      ||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1500 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1559

Qy    718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA 777
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1560 GCAACAAACATTTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1619

Qy    778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
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Db	1620	AAAATAGAAAGAAAAGAAGGCCCAAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1679
Qy	837	AACCCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCTTTTCCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAAAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTTCTGAGCTA	1496
Db	2277	TTCTCTGATTTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCTGATCATTTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCTTCCCCGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCTTCACTGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAATAGGAAAAAAGTCACTGCTTTGAC---CACCT	2513

Qy 1677 GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC 1736
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 Db 2514 GAGGGAGGAAAGCCATATTTGGAATCTTTAAGCTCAGTTTAGATAACACAAAAGATACC 2573

Qy 1737 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG 1796
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 Db 2574 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG 2633

Qy 1797 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA 1856
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 Db 2634 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA 2693

Qy 1857 AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC 1916
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 Db 2694 AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA 2753

Qy 1917 TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA 1976
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 Db 2754 TTGATCAGTTCTAAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA 2813

Qy 1977 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA 2036
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 Db 2814 GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA 2873

Qy 2037 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT 2090
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 Db 2874 GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT 2933

Qy 2091 GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA 2150
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 Db 2934 TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA 2993

Qy 2151 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT 2210
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 Db 2994 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 3053

Qy 2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
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 Db 3054 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT 3113

Qy 2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
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 Db 3114 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3173

Qy 2331 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA 2390
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 Db 3174 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA 3233

Qy 2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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 Db 3234 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3293

Qy 2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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 Db 3294 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3353


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; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1
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Query Match          58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;
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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATCTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy     121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC 891

Qy     181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCAAAGCAGAAATCTGCCGTAATAGTAGCA 951

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy     361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC 1245
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Db	2083	 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAGTGATGACTTATTTATTTCTAAGG ATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCCTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTT TGAAGAACATACAACCCAAAGTTGAAGAGAAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

|||||ng V,|||||

Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTATTGACAGTA	3099
Qy	2391	TTCAGCATTTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3579

RESULT 5

US-09-893-348-22

; Sequence 22, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

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; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22

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Query Match          58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      772 GTATTACCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy      121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db      832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAAATAC 891

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      |||||
Db      892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGCA 951

e Qy      omo 841 AATCCTTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAGTTAGTTAGTAAT 1011
      |||||
Db      952 AATCCTTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAGTTAGTTAGTAAT 1011

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      |||||
Db      1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy      361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || |||||
Db      1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy      421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      |||||
Db      1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

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Qy	481	AAAGATACTTACAAGCAAGATAGTGTGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	717
Db	1366	GATCGTCCAGGAGCATATATCATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAGAAGGCCAAATAGTAACAGAGAAGAAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCCTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCAAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376

Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACCTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATCCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCTCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTCTCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210

Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTTGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3579

RESULT 6

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1327	GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG	1386
Qy	481	AAAGATACTTACAAGCAAGATAGTGTATGTTTGTATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1387	AAAGATACTTATGAGGGAAGTAGGGAATGTGCTGGCTGCTAGAGCTAAT-----	1434
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1435	GTGGAAGGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGG	1494
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1495	AAGGATAGTGAAAGGCAGAAATGAGGATGCTTCTTTCCCGAGTACCCAGAACCTGTGAAG	1554
Qy	661	GGTGGTTCCCGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACCTGAGAATGTTTCA	720
Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCTTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Qy	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAACCTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTCATG	1139
Db	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAATAATTCTGTAGTTCCTAGTGTGGTGTCTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAATAATTCTCTCCTTCCAAGCGCTGGTGTCTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1311

Db	2152	 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT--AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	 GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT	1499
Db	2329	 TCTAATTATTTCAGAAATAGCAAAATTTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Qy	1500	GAAGATTCCCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Db	2389	 GAGGATTCCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Qy	1560	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Db	2449	 GTCCACAAAACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-	2507
Qy	1620	TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG	1679
Db	2508	-----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG	2559
Qy	1680	GGAGGAAAACCGTATTTTGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA	1739
Db	2560	 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Qy	1740	GCACCTGATGAAGTTTTCAGCATTGACCCAAAAGGAGAAAAATCCC'TTTCAGATGGAGGAG	1799
Db	2617	 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAG	2676
Qy	1800	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAITGCTCAGGAAGCAAAACCTAAGA	1859
Db	2677	 TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Qy	1860	GAAAGTGAAACATTTTTCAGATTCTCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db	2737	 GAAAGTGAAACATTTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db	2797	 GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCAGGA	2039
Db	2854	 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGCAGATTCAATTGCCTTGCTTAGAA	2913
Qy	2040	TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCGAGAT	2099
Db	2914	 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159

Db	2974	GAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Qy	2220	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	3094	GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGTGTATTG	3153
Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	3154	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213
Qy	2340	ACTGGAGTGGTGTGTTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	3214	ACTGGAGTGGTGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	3274	GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAAGGGCATAT	2519
Db	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAAGGGCATAT	3393
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAAATTCTGCTCTT	3453
Qy	2580	GGTCATGTCTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	3454	GGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Qy	2640	GATTCTCTGAAGTTTGTCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	3514	GATTCCCTGAAGTTTGTCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Db	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA	3633
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCT	2819
Db	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Qy	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC	3753
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG	2939
Db	3754	AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC---GGG	3797
Qy	2940	AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTTA	2999
Db	3798	GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTTA	3855

Qy	3000	GCAACGCAGTGTCTTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG	3059
Db	3856	GCAGTGCAGTGTCTTGAGGAAAAATGACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG	3914
Qy	3060	TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGG	3119
Db	3915	TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCAATGAGGC	3973
Qy	3120	CACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT	3179
Db	3974	GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT	4031
Qy	3180	TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCTTTTCACA	3236
Db	4032	AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAACCTTTTCACA	4091
Qy	3237	GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA	3296
Db	4092	G--TGTACTGTGTTTGGTCAGTGTAAACTGATGCAGATTTTCTGAAATGAAATGTTTA	4149
Qy	3297	GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCTTTTCTGGTATGTTCTAGG	3356
Db	4150	GATGAGAGCATACTACTAAAGCAGAGTGAAAACTCTGTC--TTTATGGTGTGTTCTAGG	4207
Qy	3357	TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA	3416
Db	4208	TGTATTGTG-AATTTACTGTTATAT----TGCCAATATAAGTAAATATAGA----CCTAA	4258
Qy	3417	TCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTT	3476
Db	4259	TCTATATATAGTGTTCACAAAGCTTAGATCTTTAACCTTGACAGCTGCCCCACAGTGCTT	4318
Qy	3477	GATACTTCTGTGCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACG	3536
Db	4319	GACCTCTGAGTCATTGGTTAT-GCAGTGTAGTCCAAGCACATAAACTAGGAAGAGAAATG	4377
Qy	3537	TACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGACGCATGCAAACAGAACT	3595
Db	4378	TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT	4437
Qy	3596	CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAACTC-----	3650
Db	4438	ATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTTTGTACAGACTCTGAAA	4497
Qy	3651	-----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA	3705
Db	4498	TTCTATGGACTGAATTTTCATGCTTCC--AAATGTTTGAGTTATCAAACATTGTTATGCA	4555
Qy	3706	AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGT	3764
Db	4556	AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAAGCCGTACTGAATT--ATCTGT	4613
Qy	3765	GGAATGCATTGTGAACTGTAAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAA	3824
Db	4614	GGAATGCATTGTGAACTGTAAAAAGCAAAGTATCAATAAAGCTTATAGATCTTAAAAA	4673

Qy 3825 AAAAAAAAAA 3833
 |||||
 Db 4674 AAAAAAAAAA 4682

RESULT 7

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US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
;   TITLE OF INVENTION:  EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE
PROGNOSIS
;   TITLE OF INVENTION:  BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH
FAVORABLE
;   TITLE OF INVENTION:  PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE
PROGNOSIS
;   FILE REFERENCE: 7388-73435
;   CURRENT APPLICATION NUMBER: US/10/220,891
;   CURRENT FILING DATE: 2003-03-07
;   PRIOR APPLICATION NUMBER: JP 2000/140387
;   PRIOR FILING DATE: 2000-05-12
;   PRIOR APPLICATION NUMBER: JP 2000/159195
;   PRIOR FILING DATE: 2000-03-07
;   NUMBER OF SEQ ID NOS: 108
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 22
;     LENGTH: 1980
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-10-220-891-22

```

Query Match 36.9%; Score 1414.6; DB 13; Length 1980;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 209; Indels 41; Gaps 9;

Qy	1326	ACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGAAGCTCCTTATATATCTATT	1385
Db	28	AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT	87
Qy	1386	GCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGT	1445
Db	88	GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGATTTCTCTGAT	147
Qy	1446	TATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTTCTGAGCTAGTTGAAGAT	1505
Db	148	TATTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTTGAAGAT	207
Qy	1506	TCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCA	1565
Db	208	TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA	267
Qy	1566	CAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCATCTGAG	1625
Db	268	CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACTTCATTTGAG	327

Qy	1626	TCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGGGAGGA	1685
Db	328	TCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCTGAGGGAGGA	384
Qy	1686	AAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAGCACCT	1745
Db	385	AAGCCATAITTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTTGTTACCT	444
Qy	1746	GATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGCTCAAT	1805
Db	445	GATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTCAGT	504
Qy	1806	ACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAGAAAAGT	1865
Db	505	ACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACT	564
Qy	1866	GAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTGTCTAGT	1925
Db	565	GAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGT	624
Qy	1926	TCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAAGTAGCCAC	1985
Db	625	CCTAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAAGTATCCAC	684
Qy	1986	AAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGATTGCCC	2045
Db	685	AAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTGCCC	744
Qy	2046	CATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCATGTCCCAGAT	2099
Db	745	CATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGAT	804
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159
Db	805	GACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCT	864
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	865	GCTTTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAA	924
Qy	2220	GCCGAGAGAAAACTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	925	GCTGAGAAAAAACTTCTTCCGATAAGAAAAAGAGACAGATCACCATCTGCTATATTT	984
Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	985	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAG	1044
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	1045	ACTGGAGTGGTGTGTTGGTGCCAGCCTATTCAGCTGCTTTTCATTGACAGTATTCAGCATT	1104
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	1105	GTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATA	1164
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTACGGGCATAT	2519

Db	1165	 TACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGGCATAT	1224
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	1225	CTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTT	1284
Qy	2580	GGTCATGTTAAGTGCACAAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	1285	GGTCATGTGAAGTGCACGATAAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTT	1344
Qy	2640	GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	1345	GATTCTCTGGAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAAT	1404
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Db	1405	GGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	1464
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	1465	CGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCT	1524
Qy	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	1525	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCA	1584
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG	2939
Db	1585	AAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGG	1639
Qy	2940	AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----AGAT	2988
Db	1640	AGGGTCAGGGAAGAACGAA-CTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGAT	1698
Qy	2989	CTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTT	3047
Db	1699	CTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTT	1758
Qy	3048	CATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTT-	3106
Db	1759	CATCATCTTAAGTATTGTAAGCTGCTATGTATGGGTTTAAACCGTAATCATATCTTTTTC	1818
Qy	3107	-TTCCTGTATGAGGCACTGGTGAATAAAACAAGATCTGAGAAAGCTGTATATTACACTTT	3165
Db	1819	CTATCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATTTTACTTT	1867
Qy	3166	GTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATA	3224
Db	1868	GTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAA	1927
Qy	3225	A 3225	
Db	1928	A 1928	

Db	1117	CTCATTTCACCTCTTCAGTGTTCCTGTATTATTTATGAACGGCATCAGGCACAGATAGATCAT	1176
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	1177	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	1236
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAAGCCTGAAAAGAGTTAACAATAGAGGAGTTT	2903
Db	1237	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC	1291
Qy	2904	ATCTTTTAAAGGGGATATTCAATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	1292	ATCTTTTAAAGGGGATATTCAATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT	1350
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTTAGCAACGCAGTG-T	3011
Db	1351	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCAGTGT	1410
Qy	3012	CTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	1411	GTGAGGAAAAATTACCTGTC'TTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	1470
Qy	3072	CTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATA	3131
Db	1471	CTATGTATGGATTTAAACCGTAATCATA--TCTTTTTCTATCTGAGGCACTGGTGAAT	1528
Qy	3132	AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGCAGGTAGTCTTGCTGTAT-TTG	3190
Db	1529	AAAAAAC-----CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG	1577
Qy	3191	GGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCCTTTTCACAGTTTGTGC	3244
Db	1578	GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGC	1637
Qy	3245	ACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA---TGTTTAGACG	3300
Db	1638	ACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACG	1697
Qy	3301	AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCTTTCCTGGTATGTTCTAGGTGTA	3360
Db	1698	AGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTA	1756
Qy	3361	TTGTGAAATTTACTGTTGTATTAAATTGCCAATATAAGTAAATATAGATTATATATATCTA	3420
Db	1757	TTGTGACTTTTACTGTTATATTAAATTGCCAATATAAGTAAATATAGATTATA-----TA	1810
Qy	3421	TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA	3480
Db	1811	TGTATAGTGTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATA	1869
Qy	3481	CT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA	3534
Db	1870	TTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGA	1929
Qy	3535	CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC	3594
Db	1930	AATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAA--ATGCCACACACATAGAAC	1986

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Qy      3595 TCC-TCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAC--AAACTCT 3651
      ||| ||||| || |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1987 TCCAACAACATCAATTTTCATTGCACAGACTGACTGTAGTTAATTTTGTACAGAATCTAT 2046

Qy      3652 GGA CTGAATCTAATGCTTCCAAAAA-----TGTTTGCAAATATCAAACATTGTTATGT 3704
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2047 GGA CTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTATGC 2106

Qy      3705 AAGAAATAT-----AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACT 3756
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2107 AAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACT 2166

Qy      3757 AAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTA 3816
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2167 AAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTA 2226

Qy      3817 AAAAAAAAAA 3825
      ||||| |||
Db      2227 AAAAAAAAAA 2235

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RESULT 9

US-10-439-388-62

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; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-62

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Query Match          23.9%;  Score 915.6;  DB 12;  Length 1785;
Best Local Similarity 85.5%;  Pred. No. 1.6e-218;
Matches 1238;  Conservative 0;  Mismatches 144;  Indels 66;  Gaps 17;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      247 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 306

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTGAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      307 CTATTCCCTGCTGCTTTCAATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACATTGCC 366

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db	367	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	426
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	427	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	486
Qy	2544	GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA	2603
Db	487	GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG	546
Qy	2604	GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	547	GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	606
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	607	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	666
Qy	2724	CTGATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	667	CTCATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	726
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC	2843
Db	727	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC	786
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTT	2903
Db	787	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC	841
Qy	2904	ATCTTTAAAGGGGATATTCAATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT	2963
Db	842	ATCTTTAAAGGGGATATTCAATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT	900
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTTAGCAACGCAGTGTC	3012
Db	901	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCAGTGTT	960
Qy	3013	-TGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	961	GTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	1020
Qy	3072	CTATGTATGGATTAAATCGTAATCATATTTGTTTTCTCTGATGAGGCACCTGGTGAATA	3131
Db	1021	CTATGTATGGATTAAACCGTAATCATA--TCTTTTTCTATCTGAGGCACCTGGTGA--	1076
Qy	3132	AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGTAT-TTG	3190
Db	1077	-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG	1127
Qy	3191	GGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCTTTTCACAGTTTGTC	3243
Db	1128	GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTC	1187
Qy	3244	CACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA----TGTTTAGAC	3299
Db	1188	CACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTGTTAGAC	1247


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;  OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-165
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Query Match 21.6%; Score 826.4; DB 13; Length 2782;
Best Local Similarity 77.6%; Pred. No. 4.9e-196;
Matches 1231; Conservative 0; Mismatches 301; Indels 54; Gaps 17;

Qy	2263	CTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT	2322
Db	1233	CTCTTCCTGCTGCATCTGAACCTGTGATACCCCTCTCTGCAGTTGTTGACCTCCTCTACT	1292
Qy	2323	GGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGCTTGTTCCTGCTGCTCTCGC	2382
Db	1293	GGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGCTTATTCCTGCTGCTGTCTC	1352
Qy	2383	TGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGA	2442
Db	1353	TGACAGTGTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA	1412
Qy	2443	CTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCC	2502
Db	1413	CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC	1472
Qy	2503	ACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAT	2562
Db	1473	ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAAT	1532
Qy	2563	ACAGCAATTCTGCTCTTGGTTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCT	2622
Db	1533	ACAGTAATTCTGCTCTTGGTTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCT	1592
Qy	2623	TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTTGATGTGGGTATTTACCTATG	2682
Db	1593	TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTTGATGTGGGTGTTTACTTATG	1652
Qy	2683	TTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTG	2742
Db	1653	TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA	1712
Qy	2743	TTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATA	2802
Db	1713	TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA	1772
Qy	2803	AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAG	2862
Db	1773	AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	1832
Qy	2863	CTGAATGAGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTC	2922
Db	1833	CAGATTGAAAAAGCC-----CCAAACAGAAGTTCATCTTTAAAGGGGACACTC	1880
Qy	2923	ATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTC	2982
Db	1881	ACTTGATTAC----GGGGGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT-	1935
Qy	2983	ACAGATCTTTATTTTATGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCT	3042

Db	1936	-CAGCTCTTTATTTTGTAGCAGTGCAGCTGTTTGAGGAAAAATTACCTGTCTTGACT-TCCT	1993
Qy	3043	GTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTT	3102
Db	1994	GTGTTTATCATCTTAAGTATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTT	2052
Qy	3103	GTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACAC	3162
Db	2053	GTCTTCCCAATGAGGCGCCTGGTGAATAAAGGAC--TCGGGGAAAGCTGTGCATTGTAT	2110
Qy	3163	TTTGTGCGAGGTAGTCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAG	3219
Db	2111	CTGCTGCGAGGGTAGTCTAGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAG	2170
Qy	3220	AAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTT	3279
Db	2171	GGAAAACCCCTTTTCACAG--TGTACTGTGTTTGGTCAGTGTAAGTGTATGCAGATTTTT	2228
Qy	3280	CTGAAATGAAATGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAGCTTGCCTT	3339
Db	2229	CTGAAATGAAATGTTTAGATGAGAGCATACTACTAAAGCAGAGTGGAAGAACTCTGTC--T	2286
Qy	3340	TCCTGGTATGTTCTAGGTGTAATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTA	3399
Db	2287	TTATGGTGTGTTCTAGGTGTATTGTG-AATTTACTGTTAT---ATTGCCAATATAAGTA	2341
Qy	3400	AATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCA	3459
Db	2342	AATATAGA----CCTAATCTATATATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCA	2397
Qy	3460	GCTGCCCCACAGTGCTTGATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACA	3519
Db	2398	GCTGCCCCACAGTGCTTGACCTCTGAGTCATTGGTTATGCAGTGTAGTCCCAAGCACATA	2457
Qy	3520	TAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGAC	3578
Db	2458	AACTAGGAAGAGAAATGTATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATAT	2517
Qy	3579	GCCATGCAAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTT	3638
Db	2518	AGAACTCCAACAAAAATATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTT	2577
Qy	3639	TATCACAAACTC-----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATA	3688
Db	2578	TGTCACAGACTCTGAAATTCTATGGACTGAATTTTCATGCTTCC--AAATGTTTGAGTTA	2635
Qy	3689	TCAAACATTGTTATGTAAGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTG	3747
Db	2636	TCAAACATTGTTATGCAAGAAATCATAAATGAAGACTTATACCATTGTGGTTTAAGCCG	2695
Qy	3748	TATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTT	3807
Db	2696	TACTGAAIT--ATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTT	2753
Qy	3808	ATAGACTTAAAAAAAAAAAAAAAAAAAAA	3833
Db	2754	ATAGACTTAAAAAAAAAAAAAAAAAAAAA	2779

US-09-765-205-5

Query Match 17.9%; Score 685.8; DB 9; Length 1610;
Best Local Similarity 88.9%; Pred. No. 6.2e-161;
Matches 831; Conservative 0; Mismatches 72; Indels 32; Gaps 7;

Qy	2304	GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGC	2363
Db	687	GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGC	746
Qy	2364	TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC	2423
Db	747	CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC	806
Qy	2424	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC	2483
Db	807	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	866
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	867	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	926
Qy	2544	GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTTCATGTTAACTGCACAATAAAA	2603
Db	927	GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTTCATGTCAACTGCACGATAAAG	986
Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	987	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	1046
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	1047	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT	1106
Qy	2724	CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	1107	CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	1166


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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156

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Query Match          17.8%; Score 683; DB 15; Length 1160;
Best Local Similarity 88.6%; Pred. No. 2.5e-160;
Matches 830; Conservative 0; Mismatches 75; Indels 32; Gaps 7;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
          |||
Db      228 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 287
          |||

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
          |||
Db      288 CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 347
          |||

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      348 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407
          |||

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      408 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 467
          |||

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTTCATGTTAACTGCACAATAAAA 2603
          |||
Db      468 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTTCATGTGAAGTGCACGATAAAG 527
          |||

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGACAGTGTTG 2663
          |||
Db      528 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGACAGTGTTG 587
          |||

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      588 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 647
          |||

Qy      2724 CTGATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          |||
Db      648 CTCATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707
          |||

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      708 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 767
          |||

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
          |||
Db      768 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA----GTAGGAGTTT 822
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[illegible]

RESULT 13

US-09-789-386-3

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; Sequence 3, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
;   APPLICANT: MICHALOVICH, DAVID
;   APPLICANT: PRINJHA, RABINDER KUMAR
;   TITLE OF INVENTION: NOVEL COMPOUNDS
;   FILE REFERENCE: GP-30165-C1
;   CURRENT APPLICATION NUMBER: US/09/789,386
;   CURRENT FILING DATE: 2001-02-21
;   PRIOR APPLICATION NUMBER: U.K. 9916898.1
;   PRIOR FILING DATE: 1999-07-19
;   PRIOR APPLICATION NUMBER: U.K. 9816024.5
;   PRIOR FILING DATE: 1998-07-22
;   PRIOR APPLICATION NUMBER: US 09/359,208
;   PRIOR FILING DATE: 1999-07-22
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 868
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (91)(413)
US-09-789-386-3

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Query Match 14.1%; Score 538.8; DB 9; Length 868;
Best Local Similarity 83.6%; Pred. No. 3e-124;
Matches 648; Conservative 0; Mismatches 118; Indels 9; Gaps 3;


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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7385
; LENGTH: 4710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7385
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[illegible]

RESULT 15

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US-09-789-386-5
; Sequence 5, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1122
; TYPE: DNA

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; ORGANISM: HOMO SAPIENS
US-09-789-386-5

Query Match 13.7%; Score 527; DB 9; Length 1122;
Best Local Similarity 95.6%; Pred. No. 3.2e-121;
Matches 542; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
          |||
Db      556 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 615

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTGAGTGTGAGTGTGAGCGTAAACAGCCCTACATTGCC 2423
          |||
Db      616 CTATTCCTGCTGCTTTTCATTGACAGTATTGAGTGTGAGCGTAAACAGCCCTACATTGCC 675

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTGAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      736 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAGTTGCTATATCT 795

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
          |||
Db      796 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 855

Qy      2604 GAACTCAGACGCCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTG 2663
          |||
Db      856 GAACTCAGGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTG 915

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      916 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 975

Qy      2724 CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          |||
Db      976 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGA 2870
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Db      1096 CCTGGATTGAAGCGTAAAGCTGAATGA 1122
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Search completed: January 23, 2004, 15:24:49
Job time : 1162.34 secs

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
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; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,662
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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          32.2%;  Score 227;  DB 4;  Length 168;
Best Local Similarity 60.0%;  Pred. No. 2.2e-19;
Matches    42;  Conservative    14;  Mismatches    14;  Indels      0;  Gaps      0;
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Qy      71 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPFRAYLESEVAISEE 130
      :|||| |::|| :|: ||||| ||||| ||||: ||:|||||:||||: :: :| |
Db      1 MLLSLAAFVSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      131 LVQKYSNSAL 140
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Db      61 AFHNYMNAAM 70
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RESULT 8

US-08-905-223-411

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; Sequence 411, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
;   APPLICANT: Edwards, Jean-Baptiste D.
;   APPLICANT: Duelert, Aymeric
;   APPLICANT: Lacroix, Bruno
;   TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
;   NUMBER OF SEQUENCES: 503
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe, Martens, Olson & Bear
;     STREET: 501 West Broadway
;     CITY: San Diego
;     STATE: California
;     COUNTRY: USA
;     ZIP: 92101-3505
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy Disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: Win95
;     SOFTWARE: Word
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/905,223
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; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -78...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

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Query Match          14.0%; Score 99; DB 3; Length 80;
Best Local Similarity 58.8%; Pred. No. 0.00017;
Matches 20; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLS--LTVFSI 80
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Db      47 VHDLI FWRDVKKTG FVFGTTLIMLLSWQLSVSSV 80

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RESULT 9

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US-09-328-352-4866
; Sequence 4866, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4866
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4866

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Query Match          10.6%; Score 75; DB 4; Length 593;
Best Local Similarity 27.5%; Pred. No. 2.1;
Matches 25; Conservative 19; Mismatches 27; Indels 20; Gaps 5;

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Qy 55 WRDIKKT--GVVFGASLFLLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIA 107
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 Db 258 WRGVKETWPAVLVGGGAFAIAQYLTSNFIGPELDPITAAIA-SLVSLTLLFRVWK----- 311
 Qy 108 IAKSDEGHPPFRAYLESEVAISEE--LVQKYS 136
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 Db 312 -----PKHIFRFEPEAGQTLAQOPTTVQRY 337

RESULT 10

US-08-853-659A-53

; Sequence 53, Application US/08853659A

; Patent No. 5925522

; GENERAL INFORMATION:

; APPLICANT: Wong, K.K.; Saffer, J.D.

; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection

; TITLE OF INVENTION: Of A

; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of
 Salmonella

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Paul W. Zimmerman

; ADDRESSEE: Intellectual Property Services

; ADDRESSEE: Battelle Memorial Institute

; ADDRESSEE: PNNL P.O. Box 999

; STREET: Washington Way

; CITY: Richland

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 99352

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage

; COMPUTER: IBM PC/XT/AT

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Word Processor (WordPerfect 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/853,659A

; FILING DATE: Unknown

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: none

; FILING DATE: n/a

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 598 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-853-659A-53

Query Match 10.3%; Score 72.5; DB 2; Length 598;

Best Local Similarity 22.5%; Pred. No. 4.1;

Matches 25; Conservative 22; Mismatches 53; Indels 11; Gaps 2;

Qy 41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLF-LLLSLTVFSIVSVTAYIALAL----- 91
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 Db 149 KKKNGRSMSSAFVLWNEFQKIKPVLNLSIFQRIADIPIFIIFLIVIVNGLGVVIVPITM 208

Qy 92 --LSVTISFRIYKGVQAIKSDGHPFRAYLESEVAISEELVQKYSNSAL 140
 :|: || : : | || | ||| :| :: :| |
 Db 209 FIVSIIISLVNHHYTNELMNKQKEGQKNRNFISEVFLSIKMIHTLNNQGL 259

RESULT 11

US-08-366-783-5

; Sequence 5, Application US/08366783

; Patent No. 5650554

; GENERAL INFORMATION:

; APPLICANT: Moloney, Maurice M

; TITLE OF INVENTION: Oil-Body Proteins As Carriers Of

; TITLE OF INVENTION: High-Value Peptides In Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DEHLINGER & ASSOCIATES

; STREET: 350 CAMBRIDGE AVENUE, SUITE 250

; CITY: PALO ALTO

; STATE: California

; COUNTRY: United States

; ZIP: 94025-1536

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/366,783

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: FABIAN, GARY

; REGISTRATION NUMBER: 33,875

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 154 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-366-783-5

Query Match 10.1%; Score 71.5; DB 1; Length 154;

Best Local Similarity 26.2%; Pred. No. 0.83;

Matches 37; Conservative 16; Mismatches 49; Indels 39; Gaps 5;

Qy 33 RSWQEMDGQKKHWKDKVVDLLYWRDIKK--TGVVFGASLFLLLSLT----- 76

| :| | : | | | | | | | :| | |

Db 6 RDQYQMSGRGSDYSKS-----RQIAKAATAVTAGGSLVLVLSLTLVGTVIALTVATPL 58

Qy 77 --VFSIVSVTAYIALALL-----SVTISFRIYKG-VIQAIKSDGHPFRAY 120

:| : | | :| | :| :| | :| :| :|

Db 59 LVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYLIEHPQGSCLKDSARMK 118

Qy 121 LESEVAISEELVQKYSNSALG 141
| | : : | | |
Db 119 LGSKAQDLKDRAQYYGQQHTG 139

RESULT 12

```

US-09-134-001C-4744
; Sequence 4744, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4744
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4744

```

Query Match 9.9%; Score 70; DB 4; Length 518;
Best Local Similarity 21.0%; Pred. No. 6.8;
Matches 21; Conservative 28; Mismatches 35; Indels 16; Gaps 4;

Qy	16	AVYSVSVGMH---NLLLLLEGRSWQEMDQKKHKWKDKVVDLLYWRDIKK---TGVVFGAS	68
		: : : : : : : : : :	
Db	400	AIVAITIAWHPNDTILNLVGNAWA---GFGAAFSPLVLVLSLYWKDLTRAGAISGMVAGAV	456
Qy	69	LFLLLSLTVFSIVSVTAYIAL-----ALLSVTISFRIYK	102
		: : : : : : : : : :	
Db	457	VVIVWISWIKPLATINAFFGMYEIIPGFIVSVLITYIVSK	496

RESULT 13

US-09-422-936-79
; Sequence 79, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-220-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 8.7;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| : | : | | : | | | : | | : | | |
Db 384 GLAWNKDDGEKESWKVKGSDSYSTRLFGEQDKKSGVALGIS 424

RESULT 15

US-08-471-733-6

; Sequence 6, Application US/08471733
; Patent No. 6068842
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,733
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE STICS: No. 1. ;175X
; LENGTH: 619 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-733-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 8.7;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| : | : ||:|: || | | : ||:| | |
Db 384 GLAWNKDDGEKESWKVGSDSYSTRLFGEQDKKSGVALGIS 424

Search completed: January 22, 2004, 16:34:54
Job time : 3.42077 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 3.84837 Seconds
(without alignments)
3523.514 Million-cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	349	49.5	208	2	I60904	neuroendocrine-spe
2	348	49.4	267	2	A60021	tropomyosin-relate
3	337	47.8	776	2	A46583	neuroendocrine-spe
4	162	23.0	2484	2	T26216	hypothetical prote
5	159	22.6	2607	2	T26215	hypothetical prote
6	158	22.4	222	2	T26213	hypothetical prote
7	83.5	11.8	295	2	S59439	probable membrane
8	81.5	11.6	464	2	C88188	protein C18H9.5 [i
9	79	11.2	618	2	T24228	hypothetical prote
10	78.5	11.1	458	2	A72258	hypothetical prote
11	77.5	11.0	261	2	F64924	probable thiosulfa
12	77.5	11.0	583	2	T49359	hypothetical prote
13	76.5	10.9	481	2	C95920	hypothetical membr

14	75.5	10.7	545	2	F64665	glucose-6-phosphat
15	74.5	10.6	545	2	E71851	glucose-6-phosphat
16	74	10.5	268	2	F64024	hypothetical prote
17	73	10.4	393	2	S67763	probable membrane
18	73	10.4	888	2	T01081	hypothetical prote
19	72.5	10.3	278	2	AD0147	probable ABC trans
20	72.5	10.3	302	2	AE2863	conserved hypothet
21	72.5	10.3	302	2	D97640	hypothetical prote
22	72.5	10.3	417	2	B96977	probable Mn transp
23	72.5	10.3	598	2	T14886	leukotoxin express
24	72	10.2	271	2	T13013	hypothetical prote
25	72	10.2	299	2	B69155	hypothetical prote
26	72	10.2	1783	2	T42386	unconventional myo
27	72	10.2	3511	2	A59295	unconventional myo
28	71.5	10.1	255	2	E84899	hypothetical prote
29	71.5	10.1	537	2	G82873	conserved hypothet
30	71	10.1	346	1	WMVZ1W	3beta-hydroxy-Delt
31	71	10.1	346	1	WMVZ2W	3beta-hydroxy-Delt
32	71	10.1	346	2	T37430	hydroxysteroid deh
33	71	10.1	476	2	B97096	2-oxoglutarate/mal
34	71	10.1	1065	2	T25068	hypothetical prote
35	70.5	10.0	153	2	AB3226	conserved hypothet
36	70.5	10.0	261	2	A90926	hypothetical prote
37	70.5	10.0	261	2	E85774	hypothetical prote
38	70.5	10.0	291	2	B69098	phosphate transpor
39	70	9.9	271	2	AC1320	hypothetical prote
40	70	9.9	619	2	S55502	membrane-associate
41	70	9.9	737	2	AE1678	heavy metal-transp
42	69.5	9.9	188	2	T04714	hypothetical prote
43	69.5	9.9	403	2	T04821	hypothetical prote
44	69.5	9.9	415	2	D95248	conserved hypothet
45	69.5	9.9	504	2	E83898	spore germination

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 49.5%; Score 349; DB 2; Length 208;
Best Local Similarity 63.4%; Pred. No. 5e-28;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

```
Qy      37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
          :|| :|| : :|||||||:|:|:|:| : || ||| ||:| || ||| ||
Db      9 KMDCVWSNWKSAIDLlyWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATI 68

Qy      97 SFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
          ||||| |:|:| |:|||||:|||| |: :|:| :|||:
Db      69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 109
```

RESULT 2

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A;Reference number: A60021; MUID:91278684; PMID:1647480

A;Accession: A60021

A;Molecule type: mRNA

A;Residues: 1-267 <WIE>

A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550

C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 49.4%; Score 348; DB 2; Length 267;
Best Local Similarity 64.0%; Pred. No. 8.4e-28;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

```
Qy      38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
          || :|| : :|||||||:|:|:|:| : || ||| ||:| || ||| ||
Db      1 MDCVWSNWKSAIDLlyWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATIS 60

Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
          ||||| |:|:| |:|||||:|||| |: :|:| :|||:
Db      61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 100
```

RESULT 3

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 47.8%; Score 337; DB 2; Length 776;
Best Local Similarity 67.4%; Pred. No. 3.5e-26;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
| | : ||||| : || : || : | | | | | : || | | : || | | | | : || :
Db 586 KQKAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 645

Qy 106 QAIKSDEGHPPRAYLESEVAISEELVQKYSN 137
|| : | : ||||| : || | | : : | : | : || : :
Db 646 QAVQKTDEGHPPKAYLELEITLSQEIQKYTD 677

RESULT 4

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 23.0%; Score 162; DB 2; Length 2484;
Best Local Similarity 31.5%; Pred. No. 7.7e-08;
Matches 34; Conservative 22; Mismatches 48; Indels 4; Gaps 1;

Qy 25 HNLLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 84

Db 2269 HSILKHHGDAWIDF----KTVPPCVLDVIYWRDAKKSIVLSLALLVLFVLAKYPLLTVV 2324
 QY 85 AYIALALLSVTISFRIFYKGVIQIAKSDEGHPFRAYLESEVAISEELV 132
 Db 2325 TYSLLLALGAAAGFRVFKKVEAOIKKTDSEHPFSEILAODLTLPOEKV 2372

RESULT 5

T26215
hypothetical protein W06A7.3a - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2607 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3a
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 22.6%; Score 159; DB 2; Length 2607;
Best Local Similarity 34.5%; Pred. No. 1.6e-07;
Matches 30; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

```

Qy      46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
      | : | : | : | | | : : | : | : : : | | | | | : : | |
Db      2409 KKEVLDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVTYSLLLALGAAAGFRVFKKVE 2468

Qy      106 QAIKSDEGHPFRAYLESEVAISEELV 132
      | | : | | | | : : : : | |
Db      2469 AOIKKTDSEHPFSEILAODLTLPOEKV 2495

```

RESULT 6

T26213
hypothetical protein W06A7.3b - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b
A;Experimental source: clone W06A7

C;Genetics:
A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 22.4%; Score 158; DB 2; Length 222;
Best Local Similarity 34.1%; Pred. No. 1.4e-08;
Matches 29; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

```
QY      48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 107
          |::|::| || | |:::| | | | |::| |
Db      26 KILDVIYWRDAKSAIVLSLALLVFLVLAKYPLLTVVITYSLLLALGAAAGFRVFKKVEAQ 85

QY      108 IAKSDEGHPFRAYLESEVAISEELV 132
          | |::| || | |:::| | |
Db      86 IKKTDSEHPFSEILAQDLTLPQEKV 110
```

RESULT 7

S59439
probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein YD9934.17c
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59439
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 <MUR>
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;
MIPS:YDR233c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;
Best Local Similarity 26.3%; Pred. No. 0.72;
Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;

```
QY      41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRI 100
          |::| | | | |:::| | | | |:::| | |
Db      12 QQQQQKSCNCDLLLWRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT----- 66

QY      101 YKGVIIQAIKSDEGHPFRAYLESEVAISEELVQKY 135
          | |:::| |:::| | |
Db      67 --GSIEFVSK-----LFLGQGLITKY 85
```

RESULT 8
C88188

protein C18H9.5 [imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C88188
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for
 investigating biology.
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and
 www.sanger.ac.uk/Projects/C_elegans/ for a list of authors
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
 1999; and Science 285, 1493, 1999
 A;Accession: C88188
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <STO>
 A;Cross-references: GB:chr_II; PID:g722384; GSPDB:GN00020; CESP:C18H9.5
 C;Genetics:
 A;Gene: C18H9.5
 A;Map position: 2

Query Match 11.6%; Score 81.5; DB 2; Length 464;
 Best Local Similarity 25.9%; Pred. No. 1.9;
 Matches 38; Conservative 28; Mismatches 50; Indels 31; Gaps 8;

```

Qy      8 VSCLRENFAVYSVSVGMHNLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFG- 66
      ::|  |  : : :|  | ::| :| :  | :|  |  |  |  |  |  |  |  |  |  |
Db     41 ITCTNANMILMNFTVICMNDVIEQKSF---SNQTHWLEKSSDISLTFSAAAVGAIFGT 96

Qy     67 ASLFLLLS-----LTVFSIVSV--TAYIALA----LLSVTISFRIYKGV-----I 105
      | :|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     97 VPAVTLISKYGIRKVLTVYGLLSAGGTLMLPLAVNYGLIPVLIA-RLFQGVGASILYSSI 155

Qy    106 QAIKS----DEGHPFRAYLESEVAIS 128
      | :|  |  :|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    156 GTISESWSPINEIGTFVAFLLSSAFQIS 182

```

RESULT 9

T24228
 hypothetical protein R166.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T24228
 R;Matthews, P.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: Z19859
 A;Accession: T24228
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-618 <WIL>
 A;Cross-references: EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166.2
 A;Experimental source: clone R166
 C;Genetics:
 A;Gene: CESP:R166.2
 A;Map position: 2

A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

Query Match 11.2%; Score 79; DB 2; Length 618;
Best Local Similarity 29.1%; Pred. No. 4.6;
Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

```
Qy      51 DLLYWRDIKK-TGVVFGASLF-LLLSLTVF-----SIVSVTAYIALAL----- 91
      |: :| : | | : : || : || || : :| || | | :
Db      353 DIQFWNNRKDLVGLSVRSVLFNIFQSLIVFLYICDNETNTMVKVTVGIGLLIECWKIPKV 412

Qy      92 LSVTISFR-IYKGVIQAIKSDGHPFRAYLESEVAISEELVQKYSNSAL 140
      ::|:| : : ||| : ||:| :|:| | ::: || ||
Db      413 MNVSIWQNKWFGVIPRLVISDKG---SYVESETKIYDQMAFKYLGWAL 458
```

RESULT 10

A72258

hypothetical protein - *Thermotoga maritima* (strain MSB8)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: A72258

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD36479.1; PID:g4981972; TIGR:TM1408

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

Query Match 11.1%; Score 78.5; DB 2; Length 458;
Best Local Similarity 26.6%; Pred. No. 3.7;
Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

```
Qy      14 NFAVY-----SVSVGMHNLNLLLEGRSWQEMDGQKKH-----WKD 47
      || : | : | || : ||
Db      196 NFLILSYLRSSIRIGFDFLL-----TRKHPQLLFIGYFYLSIWIDNFIWVKV 244

Qy      48 KVDLL-----YWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFR 99
      |::: | || | | ||| : || ||: | :|
Db      245 KGIEIAPGFFMSPEY--DIPK----FMASLFFIPSLVVFN-----LSMETVVFQR 287

Qy      100 IYKGVIQAIKSDGHPFRAYLESEVAISEELVQKYSN 137
      |||::|:| ||: | | | : :| | :||
Db      288 NYKGLMQSIV-SDK--PMRVISENLKKLSLSLRHAFSN 322
```

F64924

```
Query Match          11.0%; Score 77.5; DB 2; Length 261;  
Best Local Similarity 27.6%; Pred. No. 2.6;  
Matches    29; Conservative   16; Mismatches    43; Indels     17; Gaps      4;
```

Qy 22 VGMHNLLLLLEGRSWQE~~M~~D-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL----SLT 76
 |:| | | | | | | | | | | | | | | | | | | | :
Db 44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVLLLASGLIN 94

Qy 77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIAKSDEGHPFR 118
 |:| | | | | | | | | | | | | | | | | | | | :
Db 95 HFAMVGATAVKSLVAVHEVCGLLLACWLGFVLINAVGDNGHHYR 139

T49359

hypothetical protein B1D1.130 [imported] - *Neurospora crassa*
C;Species: *Neurospora crassa*
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49359
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-583 <SCH>
A;Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.130

A;Experimental source: BAC clone B1D1; strain OR74A
C;Genetics:
A;Gene: NCSP:B1D1.130
A;Map position: 6
A;Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.1;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

```
Qy      52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKS 111
      | | | : : : : | | | | | | : | | : | | : | | :
Db      67 LCYW-PLERRLLVLHALLLLLLLSLEHYS-----AYTRVLLHITSSINL----- 109

Qy      112 DEGHPFRAYLESEVAIS-----EELVQKYSNSALG 141
      | | : : | | : : | | : | | |
Db      110 ----PLRVLVDDEV RVAKAIAMAKDINPEELIQKRIEECAG 147
```

RESULT 13

C95920

hypothetical membrane protein [imported] - *Sinorhizobium meliloti* (strain 1021)
megaplasmid pSymB

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: C95920

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N₂-fixing endosymbiont *Sinorhizobium meliloti*.

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95920

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49027.1; PID:gl5140512; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.; Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Smb21048

A;Genome: plasmid

Query Match 10.9%; Score 76.5; DB 2; Length 481;
Best Local Similarity 37.7%; Pred. No. 6.3;
Matches 23; Conservative 8; Mismatches 27; Indels 3; Gaps 2;

```
Qy      53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD 112
      :||| | | | |||| | : | || ||: ||: ||: :: | : |
Db      238 VYWRKTKSR--VAQALAFLLLVLLLLSTSSV-AYVGLAVLSIPVALSISWSFSLGRMDKD 294

Qy      113 E 113
      |
Db      295 E 295
```

RESULT 14

F64665

glucose-6-phosphate isomerase (EC 5.3.1.9) - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999

C;Accession: F64665

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald,
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;
Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;

Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: F64665

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-545 <TOM>

A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08211.1;

PID:g2314323; TIGR:HP1166

C;Superfamily: glucose-6-phosphate isomerase

C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.1;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

```
Qy      23 GMHNLL-----LLEGRSWQEMDQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
      | | :| :||: ||: ||: | | |
Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLFKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
      :| | | :| :|| | : :||| | |
Db      465 SNILLLEKISPSNIGALVALYEHKVFFV-----QGVWDINSFDQWGVELGKELAVPILQE 519

Qy      113 -EGHPFRAYLESEVAISEELVQKYSN 137
      ||| || :| :| :| :|
Db      520 LEGHKSNAFYDSS---TKHLIELYKN 542
```

RESULT 15

E71851

glucose-6-phosphate isomerase - *Helicobacter pylori* (strain J99)

C;Species: *Helicobacter pylori*

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999

C;Accession: E71851

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.;
Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.;
Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen *Helicobacter pylori*.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: E71851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-545 <ARN>

A;Cross-references: GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AAD06664.1;

PID:g4155679

A;Experimental source: strain J99

C;Genetics:

A;Gene: *pgi*

C;Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

```

Qy      23 GMHNLL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
      | | : |           :: | : | : | | : | | : | | : | |
Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
      : | | | : : | : | | | : : | | | | | |
Db      465 SNILLEKISPSNIGALVALYEHKVFV----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy     113 -EGHPFRAYLESEVAISEELVQKYSN 137
      | | | | | : | : | : | |
Db     520 LEGHKSNA YFDSS---TRHLIELYKN 542

```

Search completed: January 22, 2004, 16:33:08

Job time : 15.8484 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 7.37604 Seconds
(without alignments)
4932.919 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Mp1450Xongth	DB	ID	rm R	Description

1	447	63.4	639	11	Q8K290	Q8k290 mus musculu
2	447	63.4	986	4	Q8IUA4	Q8iua4 homo sapien
3	447	63.4	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	447	63.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
5	443	62.8	356	11	Q8BH78	Q8bh78 mus musculu
6	443	62.8	375	11	Q8BHF5	Q8bhf5 mus musculu
7	443	62.8	392	4	Q96B16	Q96b16 homo sapien
8	436.5	61.9	1163	11	Q8K3G8	Q8k3g8 mus musculu
9	432.5	61.3	357	11	Q8K3G7	Q8k3g7 mus musculu
10	386	54.8	179	6	Q9GM33	Q9gm33 macaca fasc
11	348	49.4	199	4	Q9BQ59	Q9bq59 homo sapien
12	348	49.4	267	11	Q63765	Q63765 rattus sp.
13	337	47.8	780	11	Q8K4S4	Q8k4s4 mus musculu
14	337	47.8	780	11	Q8K0T0	Q8k0t0 mus musculu
15	325	46.1	208	13	Q90637	Q90637 gallus gall
16	320	45.4	760	13	Q90638	Q90638 gallus gall
17	308	43.7	236	11	Q8VBU0	Q8vbu0 rattus norv
18	308	43.7	237	11	Q8C6D5	Q8c6d5 mus musculu
19	308	43.7	643	11	Q8CCU2	Q8ccu2 mus musculu
20	255	36.2	234	5	Q9VMW3	Q9vmw3 drosophila
21	253	35.9	224	5	Q9VMW1	Q9vmw1 drosophila
22	252	35.7	222	5	Q9VMW4	Q9vmw4 drosophila
23	252	35.7	595	5	Q9VMV9	Q9vmv9 drosophila
24	250	35.5	202	5	Q9VMW2	Q9vmw2 drosophila
25	162	23.0	2484	5	Q9U347	Q9u347 caenorhabdi
26	159	22.6	2607	5	Q23187	Q23187 caenorhabdi
27	158	22.4	222	5	Q23188	Q23188 caenorhabdi
28	102.5	14.5	154	5	Q9VIB7	Q9vib7 drosophila
29	102.5	14.5	158	5	Q24199	Q24199 drosophila
30	85	12.1	457	10	Q8LDS3	Q8lds3 arabidopsis
31	83.5	11.8	295	3	Q04947	Q04947 saccharomyc
32	81.5	11.6	464	5	Q09484	Q09484 caenorhabdi
33	80	11.3	564	10	Q8L7Z9	Q8l7z9 spinacia ol
34	79	11.2	568	16	Q9CKM1	Q9ckm1 pasteurella
35	79	11.2	618	5	Q22003	Q22003 caenorhabdi
36	78.5	11.1	458	16	Q9X1C8	Q9x1c8 thermotoga
37	77.5	11.0	243	11	Q9JKA2	Q9jka2 mus musculu
38	77.5	11.0	798	3	Q9P6A7	Q9p6a7 neurospora
39	77	10.9	563	10	Q8L801	Q8l801 sorghum bic
40	76.5	10.9	481	16	Q92VS2	Q92vs2 rhizobium m
41	76.5	10.9	582	13	Q8AXT5	Q8axt5 salmo salar
42	76	10.8	563	10	Q9FMF7	Q9fmf7 arabidopsis
43	75.5	10.7	246	11	Q9JKA0	Q9jka0 mus musculu
44	75	10.6	255	10	Q9SH59	Q9sh59 arabidopsis
45	74.5	10.6	294	16	Q8D716	Q8d716 vibrio vuln

ALIGNMENTS

RESULT 1

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.

AC Q8K290;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)


```

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; AY102285; AAM64244.1; -.
DR EMBL; AY123245; AAM64249.1; -.
DR EMBL; AY123246; AAM64250.1; -.
DR EMBL; AY123247; AAM64251.1; -.
DR EMBL; AY123248; AAM64252.1; -.
DR EMBL; AY123249; AAM64253.1; -.
DR EMBL; AY123250; AAM64254.1; -.
SQ SEQUENCE 986 AA: 108449 MW: 0CDE8F647036415A CRC64;

```

Qy 46 KDKVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 796 KTSVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 855

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 856 OAIOKSDEGHPFRAYLESEVAISEELVQKYSNSALG 891

RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102280; AAM73502.1; -.
 DR EMBL; AY102286; AAM73507.1; -.
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 1046;
 Best Local Similarity 96.9%; Pred. No. 8.6e-37;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
 | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 856 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 915
 Qy 106 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||| ||||||||||||||||||||||||||||||||
 Db 916 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 951

RESULT 4

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.
 AC Q8BGM9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102284; AAM73506.1; -.
 DR EMBL; AY102286; AAM73511.1; -.
 SQ SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

Query Match 63.4%; Score 447; DB 11; Length 1162;
 Best Local Similarity 96.9%; Pred. No. 9.6e-37;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
 | |||||
 Db 972 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031
 Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||| |||||
 Db 1032 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1067

RESULT 5

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.
 AC Q8BH78;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102281; AAM73503.1; -.

DR EMBL; AY102286; AAM73508.1; -.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 356;
Best Local Similarity 98.9%; Pred. No. 6.6e-37;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
          |||
Db      169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 261
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RESULT 6

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.
AC Q8BHF5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RTN4.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102282; AAM73504.1; -.
DR EMBL; AY102286; AAM73509.1; -.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 375;
Best Local Similarity 98.9%; Pred. No. 7e-37;

Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
          |||
Db      188 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 247

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      248 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 280
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RESULT 7

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia ~~Primate~~ Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Pr; *p725Xn
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.

Query Match 62.8%; Score 443; DB 4; Length 392;
Best Local Similarity 98.9%; Pred. No. 7.4e-37;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ID      Q8K3G8                PRELIMINARY;          PRT;   1163 AA.
AC      Q8K3G8;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23,      t annotation update)
DE      Nogo-A.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Jin W., Long M., Li R., Ju G.;
RT      "Cloning and expression of the mouse Nogo-A protein.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY114152; AAM77068.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

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Query Match 61.9%; Score 436.5; DB 11; Length 1163;
Best Local Similarity 95.9%; Pred. No. 1.1e-35;
Matches 93; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

ID O8K3G7 PRELIMINARY; PRT; 357 AA.

AC Q8K3G7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nogo-B.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RT "Cloning and expression of the mouse Nogo-B protein."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114153; AAM77069.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match p2125X561.3%; Score 432.5; DB 11; Length 357; G ;875X
 Best Local Similarity 97.9%; Pred. No. 7.8e-36;
 Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 49 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 107
 |||
 Db 169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 228

 Qy 108 IAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |
 Db 229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 262

RESULT 10

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.
 AC Q9GM33;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 19.9 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

RESULT 12

Q63765

ID Q63765 PRELIMINARY; PRT; 267 AA.
AC Q63765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat C1-13 gene product.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD; TISSUE=Brain;
RX MEDLINE=91278684; PubMed=1647480;
RA Wieczorek D.F., Hughes S.R.;
RT "Developmentally regulated cDNA expressed exclusively in neural
RT tissue.";
RL Brain Res. Mol. Brain Res. 10:33-41(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD; TISSUE=Brain;
RA Wieczorek D.F.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X52817; CAA37001.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 267 AA; 30328 MW; A591C6E37DB7A175 CRC64;

Query Match 49.4%; Score 348; DB 11; Length 267;
Best Local Similarity 64.0%; Pred. No. 2.3e-27;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
|| :|| : :|||||||:|:|:| : || ||| ||:| ||| ||| |||
Db 1 MDCVWSNWKSQ AIDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALASATIS 60
Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
|||| |:|: |:|||||:|||| |: :|: :| ||:|
Db 61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 100

RESULT 13

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.
AC Q8K4S4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Reticulon 1A.
GN RTN1 OR RTN-1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,
 RA Osumi N.;
 RT "Mosaic development of the olfactory cortex with Pax6-dependent and
 RT -independent components.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB074899; BAB96551.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 47.8%; Score 337; DB 11; Length 780;
 Best Local Similarity 67.4%; Pred. No. 1e-25;
 Matches 62; Conservative 16; iXMismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 105
 | | : ||||| ||| : ||| : | || ||| ||| : ||| ||| : ||| ||| ||||| | :
 Db 590 KQKAIDLLYWDRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 649
 Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
 || : | : ||||| : ||| | : : | : ||| : :
 Db 650 QAVQKTDEGHPFKAYLELEITLSQEIQKYTD 681

RESULT 14

Q8K0T0

ID Q8K0T0 PRELIMINARY; PRT; 780 AA.
 AC Q8K0T0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to reticulon 1.
 GN RTN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10 TI
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030455; AAH30455.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.

Query Match 47.8%; Score 337; DB 11; Length 780;
Best Local Similarity 67.4%; Pred. No. 1e-25;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

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Qy      46 KDKVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 105
      | | : ||||| | | : || | : | | | | | : || | | : || | | | | | | | :
Db      590 KQKAIDL LLYWRDIKQTGIVFGSFL LLL LFSLTQFSVVS VVAYLALAALSATISFRIYKSVL 649
      *
Qy      106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
      | | : | : ||||| | : || | | : : | : | : || | : :
Db      650 QAVOKTDEGHPFKAYLELEITLSQEIQKYTD 681

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090637

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ID      Q90637          PRELIMINARY;          PRT;    208 AA.
AC      Q90637;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, La t annotation update)
DE      ChS-Rex-s.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=96386034; PubMed=8793864;
RA      Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
RA      Georgiev G.P., Buchman V.L.;
RT      "Intracellular compartmentalization of two differentially spliced s-
RT      rex/NSP mRNAs in neurons.";
RL      Mol. Cell. Neurosci. 7:289-303(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=97183663;
RA      Ninkina N.N., Baka I.D., Buchman V.L.;
RT      "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
RT      transcripts and expression of splice variants in rat tissues.";
RL      Gene 184:205-210(1997).
DR      EMBL; U17605; AAC60074.1; -.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE    208 AA;  23593 MW;  9C90FDAEE15DAB45 CRC64;

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Query Match 46.1%; Score 325; DB 13; Length 208;
Best Local Similarity 59.4%; Pred. No. 3.8e-25;
Matches 60; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 37 EMDGQKKHWDKDVVDLLVWRDI KKTGVVFVGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
 :|| : || : :: ||| | : || : || : || : || : || : || : || : || : || : ||

Db 9 KMDCLWSNWKCQAINLLYWREIKQTGIVFGSLLLLLLFSLTQFSVSVVAYLALAGLSATI 68

Qy 97 SFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137

||||| |:|: |:|||||:|: |: :|: :|:|:|:

Db 69 SFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQDQIQKYTD 109

Search completed: January 22, 2004, 16:34:13

Job time : 8.37604 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:34:19 ; Search time 6.94845 Seconds
(without alignments)
4195.163 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	510	72.3	199	9	US-09-893-348-21	Sequence 21, Appl
2	503	71.3	118	12	US-10-264-237-1568	Sequence 1568, Ap
3	503	71.3	199	9	US-09-893-348-25	Sequence 25, Appl
4	447	63.4	1163	9	US-09-893-348-18	Sequence 18, Appl
5	447	63.4	1192	9	US-09-789-386-2	Sequence 2, Appli
6	447	63.4	1192	9	US-09-758-140-6	Sequence 6, Appli
7	447	63.4	1192	9	US-09-893-348-23	Sequence 23, Appl
8	447	63.4	1192	9	US-09-972-599A-6	Sequence 6, Appli
9	447	63.4	1192	15	US-10-060-036-71	Sequence 71, Appl
10	443	62.8	360	9	US-09-893-348-20	Sequence 20, Appl
11	443	62.8	373	9	US-09-789-386-6	Sequence 6, Appli
12	443	62.8	373	9	US-09-765-205-6	Sequence 6, Appli
13	443	62.8	373	9	US-09-893-348-24	Sequence 24, Appl
14	443	62.8	373	15	US-10-060-036-72	Sequence 72, Appl
15	443	62.8	379	12	US-10-205-194-164	Sequence 164, App
16	348	49.4	267	12	US-10-205-194-127	Sequence 127, App
17	337	47.8	777	12	US-10-205-219-93	Sequence 93, Appl
18	309	43.8	236	9	US-09-729-674-20	Sequence 20, Appl
19	309	43.8	236	9	US-09-765-205-26	Sequence 26, Appl
20	309	43.8	269	15	US-10-106-698-6222	Sequence 6222, Ap
21	304	43.1	593	12	US-10-108-260A-2892	Sequence 2892, Ap
22	269	38.2	161	9	US-09-925-302-808	Sequence 808, App
23	227	32.2	168	11	US-09-809-391-563	Sequence 563, App
24	227	32.2	168	12	US-09-882-171-563	Sequence 563, App
25	213	30.2	66	9	US-09-758-140-20	Sequence 20, Appl
26	213	30.2	66	9	US-09-972-599A-20	Sequence 20, Appl
27	207	29.4	66	9	US-09-972-599A-22	Sequence 22, Appl
28	207	29.4	66	11	US-09-972-546-7	Sequence 7, Appli
29	193	27.4	40	9	US-09-758-140-8	Sequence 8, Appli
30	193	27.4	40	9	US-09-758-140-18	Sequence 18, Appl
31	193	27.4	40	9	US-09-972-599A-18	Sequence 18, Appl
32	177	25.1	72	12	US-10-029-386-28762	Sequence 28762, A
33	156.5	22.2	36	9	US-09-972-599A-28	Sequence 28, Appl
34	155.5	22.1	36	9	US-09-972-599A-30	Sequence 30, Appl
35	135.5	19.2	31	9	US-09-972-599A-32	Sequence 32, Appl
36	133.5	18.9	31	9	US-09-972-599A-26	Sequence 26, Appl
37	125	17.7	25	9	US-09-972-599A-8	Sequence 8, Appli
38	123	17.4	25	9	US-09-972-599A-24	Sequence 24, Appl
39	118	16.7	25	9	US-09-758-140-10	Sequence 10, Appl
40	118	16.7	25	9	US-09-972-599A-10	Sequence 10, Appl
41	115.5	16.4	26	9	US-09-972-599A-34	Sequence 34, Appl
42	113	16.0	25	9	US-09-758-140-12	Sequence 12, Appl
43	113	16.0	25	9	US-09-972-599A-12	Sequence 12, Appl
44	81.5	11.6	464	12	US-10-369-493-5428	Sequence 5428, Ap
45	72.5	10.3	714	12	US-10-369-493-3467	Sequence 3467, Ap

ALIGNMENTS

RESULT 1
 US-09-893-348-21
 ; Sequence 21, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal

```
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21
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Query Match          72.3%; Score 510; DB 9; Length 199;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      38 MDGQKKHKWVKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
          |||
Db      1 MDGQKKHKWVKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      61 FRIYKGVIAIAKQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
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RESULT 2

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US-10-264-237-1568
; Sequence 1568, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1568
; LENGTH: 118
; TYPE: PRT
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          |||||:|||||
Db      1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||||
Db      61 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

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RESULT 4

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US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

```

```

Query Match          63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 8.3e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
          | |||||
Db      973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1032

Qy      106 QAIKSDGEGH1475Xv EVAISEELVQKYSNSALG 141
          ||| |||||
Db      1033 QAIQKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 1068

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RESULT 5

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US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:

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Query Match 63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.6e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      46 KDKVVDLLYWRDIKKTGVVFVGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI   105
       | |||||||
Db     1002 KTSVVDLLYWRDIKKTGVVFVGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI   1061

Qy      106 QAIAKSDEGHPPFRAYLESEVAISEELVQKYNSALG    141
        |||||
Db     1062 QAIOKSDEGHPPFRAYLESEVAISEELVQKYNSALG    1097
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RESULT 7

```

US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

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Query Match 63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.6e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

RESULT 8

US-09-972-599A-6

; Sequence 6, Application US/09972599A
 ; Patent No. US20020077295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STRITTMATTER, STEPHEN M.
 ; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
 ; FILE REFERENCE: C077 CIP US
 ; CURRENT APPLICATION NUMBER: US/09/972,599A
 ; CURRENT FILING DATE: 2001-10-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: 09/758,140
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: 60/236,378
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/207,366
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/175,707
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-599A-6

Query Match 63.4%; Score 447; DB 9; Length 1192;
 Best Local Similarity 96.9%; Pred. No. 8.6e-43;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
 | |||||
 Db 1002 KTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1061
 Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||| |||||
 Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 9

US-10-060-036-71

; Sequence 71, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 ; FILE REFERENCE: 210121.566
 ; CURRENT APPLICATION NUMBER: US/10/060,036

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; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71
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Query Match 63.4%; Score 447; DB 15; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.6e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

RESULT 10

US-09-893-348-20

; Sequence 20, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

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; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 20

; LENGTH: 360

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; TYPE: PRT
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; ORGANISM: Rattus norvegicus

US-09-893-348-20

Query Match 62.8%; Score 443; DB 9; Length 360;
Best Local Similarity 98.9%; Pred. No. 5.1e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 232

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
      ||||||||||||||||||||||||||||||||||||
Db      233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 265

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RESULT 11

US-09-789-386-6

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; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6

```

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Query Match          62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
      ||||||||||||||||||||||||||||||||||||
Db      246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

```

RESULT 12

US-09-765-205-6

```

; Sequence 6, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17

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; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6

Query Match 62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
|||||
Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
|||||
Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 13

US-09-893-348-24

; Sequence 24, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

Query Match 62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 14

US-10-060-036-72

; Sequence 72, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 ; FILE REFERENCE: 210121.566
 ; CURRENT APPLICATION NUMBER: US/10/060,036
 ; CURRENT FILING DATE: 2002-01-30
 ; NUMBER OF SEQ ID NOS: 4560
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-060-036-72

Query Match 62.8%; Score 443; DB 15; Length 373;
 Best Local Similarity 98.9%; Pred. No. 5.4e-43;
 Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 15

US-10-205-194-164

; Sequence 164, Application US/10205194
 ; Publication No. US20030134301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alistair
 ; APPLICANT: Brooksbank, Robert
 ; APPLICANT: Pinnock, Robert

```

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164

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```

Query Match          62.8%; Score 443; DB 12; Length 379;
Best Local Similarity 98.9%; Pred. No. 5.5e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      192 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 251

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          ||||||||||||||||||||||||||||
Db      252 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 284

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Job time : 7.94845 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 2.35178 Seconds
(without alignments)
2819.465 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSAIG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	495	70.2	199	1	RTN4_MOUSE	Q99p72 mus musculu
2	447	63.4	1163	1	RTN4_RAT	Q9jk11 rattus norv
3	447	63.4	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
4	337	47.8	776	1	RTN1_HUMAN	Q16799 homo sapien
5	337	47.8	777	1	RTN1_RAT	Q64548 rattus norv
6	309	43.8	236	1	RTN3_HUMAN	O95197 homo sapien
7	308	43.7	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	214	30.4	545	1	RTN2_HUMAN	O75298 homo sapien
9	197	27.9	471	1	RTN2_MOUSE	O70622 mus musculu
10	77.5	11.0	243	1	T2RD_MOUSE	Q9jka2 mus musculu
11	77.5	11.0	261	1	PHSC_ECOLI	P77409 escherichia
12	75.5	10.7	246	1	T2R8_MOUSE	Q9jka0 mus musculu
13	75.5	10.7	545	1	G6PI_HELPY	O25781 helicobacte
14	74.5	10.6	545	1	G6PI_HELPJ	Q9zk49 helicobacte
15	74	10.5	268	1	YC73_HAEIN	P44150 haemophilus
16	72	10.2	614	1	S6AC_RABIT	P48055 oryctolagus
17	72	10.2	3511	1	MY15_MOUSE	Q9qzz4 mus musculu

18	71	10.1	346	1	3BHS_VACCC	P21097	v 3 beta-hy
19	71	10.1	346	1	3BHS_VACCV	P26670	v 3 beta-hy
20	70	9.9	960	1	GBR1_MOUSE	Q9wv18	mus musculu
21	70	9.9	961	1	GBR1_HUMAN	Q9ubs5	homo sapien
22	70	9.9	991	1	GBR1_RAT	Q9z0u4	rattus norv
23	69	9.8	315	1	LXD1_PHOLE	P21309	photobacter
24	69	9.8	398	1	PGK_STRPN	Q97s89	streptococc
25	69	9.8	468	1	YDBM_CAEEL	Q19084	caenorhabdi
26	68.5	9.7	238	1	T2RA_MOUSE	Q9jka3	mus musculu
27	68.5	9.7	311	1	HTRB_HAEIN	P45239	haemophilus
28	68.5	9.7	325	1	VP35_VARV	P33059	variola vir
29	68	9.6	184	1	YDB5_SCHPO	Q10358	schizosacch
30	68	9.6	1447	1	DCC_HUMAN	P43146	homo sapien
31	67.5	9.6	324	1	VP35_VACCC	P20497	vaccinia vi
32	67.5	9.6	503	1	LEU1_BUCUM	Q9evh0	buchnera ap
33	67.5	9.6	877	1	SULH_SCHPO	O74377	schizosacch
34	67	9.5	175	1	OLE2_BRANA	P29111	brassica na
35	67	9.5	453	1	SYS_ARCFU	O28244	archaeoglob
36	67	9.5	525	1	SYH_CAEEL	P34183	caenorhabdi
37	67	9.5	756	1	RIR1_HAEIN	P43754	haemophilus
38	66.5	9.4	3174	1	CHAC_HUMAN	Q96rl7	homo sapien
39	66	9.4	253	1	ADH_DROAD	Q00669	drosophila
40	66	9.4	537	1	YCUB_SCHPO	O59831	schizosacch
41	66	9.4	548	1	AMDS_EMENI	P08158	emer icella
42	65.5	9.3	182	1	Y696_METJA	Q58107	methanococc
43	65.5	9.3	664	1	NTPI_ENTHR	P43439	enterococcu
44	65.5	9.3	880	1	DPO1_BACSU	O34996	bacillus su
45	65.5	9.3	1037	1	YOJ8_YEAST	Q12496	saccharomyc

ALIGNMENTS

RESULT 1

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99P72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN RTN4 OR NOGO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RT "Mouse vp20/RTN4C cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,